

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 22, 2004, 16:52:22 ; Search time 139 seconds  
(without alignments)  
7433.654 Million cell updates/sec

Title: US-09-991-053-9

Perfect score: 2341  
Sequence: 1 cactcccccttctgtat.....ttaagacaaagtcataaa 2341

Scoring table: IDENTITY NUC  
Gapop 10-0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2171.8	92.8	2185	US-09-996-243-228	Sequence 228, App
2	605	25.8	2906	US-09-996-243-500	Sequence 500, App
3	439.8	18.8	973	US-09-482-273-13	Sequence 13, App1
4	430	18.4	984	US-09-482-273-82	Sequence 82, App1
5	108.8	4.6	2019	US-09-063-950-3	Sequence 3, App1
6	108.8	4.6	2768	US-09-996-243-51	Sequence 51, App1
7	108.8	4.6	2852	US-09-063-950-1	Sequence 1, App1
8	85.4	3.6	1685	5340934-1	Sequence 1, App1
9	80.6	3.4	2724	US-09-170-496D-263	Sequence 263, App
10	80.6	3.4	2724	US-09-170-496D-277	Sequence 277, App
11	77	3.3	4843	US-08-986-485-1	Sequence 1, App1
12	75.8	3.2	5176	US-09-182-024A-1	Sequence 1, App1
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14	71.8	3.1	1777	US-09-620-312D-92	Sequence 92, App1
15	66.8	2.9	7452	US-09-461-325-40	Sequence 40, App1
16	66.8	2.9	7452	US-08-592-500-1	Sequence 1, App1
17	66.8	2.9	7452	US-08-195-006-1	Sequence 1, App1
18	66.2	2.8	4104	PCT-US94-07644A-1	Sequence 1, App1
19	63.6	2.7	8378	US-09-996-243-277	Sequence 277, App
20	62	2.6	3747	PCT-US91-08055-1	Sequence 1, App1
21	62	2.6	3837	US-10-042-810-1	Sequence 1, App1
22	62	2.6	3837	US-10-042-810-3	Sequence 3, App1
23	56	2.4	4068	US-10-042-810-5	Sequence 5, App1
24	52.8	2.3	3083	US-09-484-970B-169	Sequence 169, App
25	50	2.1	50	US-09-996-243-251	Sequence 251, App
26	49.8	2.1	2159	US-08-286-870A-7	Sequence 7, App1
27	49.6	2.1	2082	US-08-985-335-4	Sequence 4, App1

ALIGNMENTS

28	49.6	2.1	2082	3	US-09-410-372-4	Sequence 4, App1
29	49.2	2.1	5583	4	US-09-312-283C-372	Sequence 372, App
30	48.6	2.1	2636	1	US-08-156-020-3	Sequence 3, App1
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35	48.2	2.1	1600	1	US-08-483-043-12	Sequence 12, App1
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RESULT 1  
US-09-996-243-228  
Sequence 228, Application US/09996243  
Patent No. 6478825  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Ecton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gueney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Peoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C13  
CURRENT APPLICATION NUMBER: US/09/996, 243  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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73	PRIOR FILING DATE: 1998-07-02

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 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

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Db 2101 TTTCTGTATATGCTTATATATTAAGTCTATGGCTGGTTAAAAAACAATTTATTTAA 2160  
Qy 2319 AATTTAAGCAAAAAGTCAAAA 2341  
Db 2161 AATTTAAGCAAAAAGTCAAAA 2183

RESULT 2  
US-09-996-243-500  
Sequence 500, Application US/09996243  
Patent No. 6478825  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyer, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottlieb, Audrey E.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gutney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas P.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C13  
CURRENT APPLICATION NUMBER: US/09/996,243  
PRIORITY FILING DATE: 2001-11-14  
PRIORITY APPLICATION NUMBER: 60/049787  
PRIORITY FILING DATE: 1997-06-16  
PRIORITY APPLICATION NUMBER: 60/062250  
PRIORITY FILING DATE: 1997-10-17  
PRIORITY APPLICATION NUMBER: 60/065186  
PRIORITY FILING DATE: 1997-11-12  
PRIORITY APPLICATION NUMBER: 60/065311  
PRIORITY FILING DATE: 1997-11-13  
PRIORITY APPLICATION NUMBER: 60/066770  
PRIORITY FILING DATE: 1997-11-24  
PRIORITY APPLICATION NUMBER: 60/075945  
PRIORITY FILING DATE: 1998-02-25  
PRIORITY APPLICATION NUMBER: 60/078910  
PRIORITY FILING DATE: 1998-03-20  
PRIORITY APPLICATION NUMBER: 60/083322  
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PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089907  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089908  
PRIOR FILING DATE: 1998-06-18

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AR252532  
 DEFINITION AR252532 2185 bp DNA linear PAT 20-DEC-2002  
 SEQUENCE 228 from patent US 6478825.  
 ACCESSION AR252532  
 VERSION AR252532.1 GI:27300440  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 2185)  
 Winterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.  
 Authors Implant, method of making same and use of the implant for the  
 Title treatment of bone defects  
 Journal Patent: US 6478825-A 228 12-NOV-2002;  
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 Pred. No.: 2.07e-271 Length: 2185  
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Db	957	CTTTGAACTGTGATTTGTGACATTTCTGTGCTAGCCCTGGGCTTGGAGATTAATACC		1016
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OY	341	ValGIuValApeGIuAlaSerPheGIuCysSerAlaProPheIleMetAspAlaProArg		360
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Db	1317	GTTTACACATCATGTGTGACCAATGTGCGAGGCACTCCACGCTCGGCTCAACTCAAT		1376
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 AC AAX90848;  
 DT 17-JAN-2000 (first entry)  
 DE cdna clone cc359\_4.  
 XX clone cc359\_4; cc359\_4 protein; human adult brain cdna library;  
 KW secreted protein; H23117; human cdna clone 51970 3'; gene therapy;  
 KW cytokine; nutritional activity; cell proliferation; immune stimulation;  
 KW immune suppression; hematopoiesis regulation; tissue growth;  
 KW tumour inhibition; ds.  
 XX Homo sapiens.  
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 FH Key Location/Qualifiers  
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 FT /product= "cc359\_4 protein"  
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 FT mat\_peptide 339..2177  
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 XX W0950405-A1.  
 PD 07-OCT-1999.  
 XX  
 PF 30-MAR-1999; 99WO-US06946.  
 XX  
 PR 31-MAR-1998; 98US-0080110.  
 PR 29-MAR-1999; 99US-0280591.  
 XX  
 PA (GENE) GENETICS INST INC.  
 XX  
 PI Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;  
 PI Merberg D, Treacy M, Agostino MJ, Steinhilber RJ;  
 XX  
 DR WPI: 1999-610849/52.  
 DR P-PSDB; AAY28806.  
 XX  
 PT Polynucleotides encoding secreted human proteins, derived from human  
 PT adult brain, human fetal brain, human fetal kidney, and human adult  
 PT blood cdna libraries  
 XX  
 PS Claim 1; Page 96-97; 122pp; English.  
 XX  
 CC The present nucleotide sequence comprises the full-length protein-coding  
 CC sequence of clone cc359\_4. cc359\_4 was isolated from a human adult brain  
 CC cdna library using methods specific for secreted protein cdnas. This  
 CC demonstrates some similarity with AAY23117 of human cdna clone 51970 3'.  
 CC This can be used in gene therapy. The polynucleotide and protein may  
 CC effect nutritional activity, cytokine and cell proliferation, immune  
 CC stimulation or suppression, hematopoiesis regulation, tissue growth,  
 CC tumour inhibition etc.  
 CC  
 SQ Sequence 2360 BP; 582 A; 707 C; 562 G; 508 T; 1 other;  
 Query Match 98.9%; Score 2316.2; DB 20; Length 2360;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 2332; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
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 Db 2 CACTTCCCTTTTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 61  
 Qy 61 CCGTGAAGAAAGCTTAAGACACCAAGCAGTGTCTTCCCTTCCCTGAGATGAA 120  
 Db 62 CCGTGAAGAAAGCTTAAGACACCAAGCAGTGTCTTCCCTTCCCTGAGATGAA 121  
 Qy 121 AGAGAGCTCTTACCTCACTTAAGCCGAGGATGAGGCTTCTCTTCCAGACCAAAAT 180

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1981 TGTATCAAGTGAACAGACATCCGCAAGACATCCGCAAGACATCCGCAAGACAT 2040  
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2101 CACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160  
2102 CACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2161  
2161 GGAATCTCACTTGGCCCAATTAATCTTCTTGGCCCAATTAATCTTGGCCCAAT 2220  
2162 GGAATCTCACTTGGCCCAATTAATCTTCTTGGCCCAATTAATCTTGGCCCAAT 2220  
2221 AAAGACAGCACTTTTGTGACAGAGTGGGAGAGCTTTTGTGACAGAGTGGGAG 2280  
2222 AAAGACAGCACTTTTGTGACAGAGTGGGAGAGCTTTTGTGACAGAGTGGGAG 2280  
2281 AAGTCTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340  
2282 AAGTCTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340

$$\begin{array}{l} \text{ }^n \text{ }? f \tau \leq \cdot \blacksquare \Delta ? f \tau \leq \cdot \blacksquare \text{ } \otimes ? \blacksquare \blacktriangle \nabla \Delta \blacksquare ? \mathring{A} \cap \parallel \approx f \cdot n \pm \\ \circ \sim \nabla \vdash \beta \equiv n > \nabla \vdash \beta \equiv \blacksquare \text{ } \otimes ? \blacksquare \nabla \nabla \Delta^n \nabla \hat{a} f \perp \perp^n \Delta^n \cdot \pm \\ f \sqrt{\perp} \mathring{A} \parallel \leq \pi \cdot \nabla^n \text{ } \parallel \circ \sim \nabla \vdash \beta \equiv n > \nabla \vdash \beta \equiv \blacksquare ? \blacksquare \blacktriangle \Delta \alpha \heartsuit \mathcal{L} \Delta \alpha ? \leq \pm \\ \text{ } ? \leq \blacksquare > \end{array}$$



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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 22, 2004, 20:06:15 ; Search time 459 seconds  
(without alignments)  
3840.377 Million cell updates/sec

Title: US-09-991-053-10  
Perfect score: 3446  
Sequence: 1 MKLLMQVYVHHTWNAILLP.....ISEPYYIQTHKDKVQETQI 653

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues  
Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-DB=N.Geneseq.19Jun03 -QMT=faetap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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25: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	* Match Length	DB	ID	Description
1	3446	100.0	2341	21	AAA93620 Human SLIT protein
2	3407	98.9	1962	22	AAD16345 Human SH3BP331a g
3	3407	98.9	2185	21	AAC58383 Human PRO1111 nucl
4	3407	98.9	2185	21	AAZ65033 Membrane-bound pro
5	3407	98.9	2185	22	AA521462 Human cDNA sequenc
6	3407	98.9	2185	22	AA441719 Human PRO1111 (UNQ
7	3407	98.9	2185	25	ACA03821 cDNA encoding huma
8	3407	98.9	2185	25	ABX78858 Human cDNA encodin
9	3407	98.9	2185	25	ABX89359 Novel human secret
10	3407	98.9	2185	25	ABX80270 Human secreted/ltra
11	3407	98.9	2185	25	ABX80774 Novel human secret
12	3407	98.9	2185	25	ABX81157 Human secreted/ltra
13	3407	98.9	2185	25	ABX79454 Human PRO polynuc
14	3407	98.9	2185	25	ABX79454 Human secreted/ltra
15	3407	98.9	2185	25	ABX64093 cDNA encoding huma
16	3407	98.9	2185	25	ABX17057 Human PRO polynuc
17	3407	98.9	2185	25	ABX17057 cDNA clone cc359.4
18	3398	98.6	2360	20	AAA93621 Human SLIT protein
19	3253	94.4	2607	21	AAA93621 Human immunoglobul
20	3148	91.4	2324	22	AAA93621 Human cDNA SEQ ID
21	2855	82.6	2159	22	ABA06571 Human cDNA sequenc
22	2855	82.6	2159	24	ABV83908 Human SLIT protein
23	2356	68.4	1356	21	AAA93631 Human OREF ORF2855
24	2284	66.3	1805	21	AAC77300 Human cDNA SEQ ID
25	1954	56.7	1168	22	ABA06744 Human immunoglobul
26	1954	56.7	1168	22	ABA06744 Human polynucleoti
27	1954	56.7	1168	24	ABV84081 DNA encoding human
28	1898	55.1	2316	25	ABX70472 Human cDNA encodin
29	1898	55.1	2397	22	AAK62093 Human leucine-rich
30	1898	55.1	2493	24	AAAD2187 Human cDNA encoding
31	1898	55.1	2756	24	ABX03577 Human cDNA encodin
32	1898	55.1	3027	24	ABK62087 Human PRO331 DNA E
33	1832	53.2	2095	20	AAK37738 Novel nucleotide s
34	1832	53.2	2851	20	AAK08687 Protein PRO331 cDN
35	1832	53.2	2906	20	AAK52655 Human PRO331 cDNA
36	1832	53.2	2906	21	AAK77596 Human PRO331 prote
37	1832	53.2	2906	21	AAK521427 Human cDNA sequenc
38	1832	53.2	2906	22	AAK500162 Human cDNA clone D
39	1832	53.2	2906	22	AAK72423 Human PRO331 cDNA
40	1832	53.2	2906	22	AAK72423 Human PRO331 nucle
41	1832	53.2	2906	22	AAK94745 Human angiogenesis
42	1832	53.2	2906	25	ACA55048 Novel human secret
43	1832	53.2	2906	25	ACA55048 cDNA encoding huma
44	1832	53.2	2906	25	ACA55048 Human cDNA for sec
45	1832	53.2	2906	25	ACA60240

## ALIGNMENTS

RESULT 1  
AAA93620 standard; DNA; 2341 BP.  
AAA93620;  
16-JAN-2001 (first entry)  
Human SLIT protein-like splice variant SECC 3352358-1 DNA.  
SECC protein; human; secreted; membrane-associated; cancer;  
proliferation regulator; differentiation regulator; non-malignant tumour;  
immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;  
infection; inflammatory disorder; arthritis; haematopoietic disorder;  
skin disorder; cardiovascular disorder; atherosclerosis; restenosis;  
neurological disease; Alzheimer's disease; trauma; wounding;  
spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;

KM anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic;  
 KM neuroprotective; vulnerary; antiallergic; antimicrobial; cardiant;  
 KM dermatological; gene therapy; ds.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FT CDS 214..2299  
 FT /\*tag= a  
 FT /product= "Human SECX 3352358-1 protein"  
 FT /transl\_except= (pos:2174..2176, aa:Xaa)  
 FT /note= "Xaa = unknown. Base 2174-2176 correspond to an  
 in-frame stop codon"  
 FT  
 XX MO200053742-A2.  
 PN  
 XX 14-SEP-2000.  
 PD  
 XX 09-MAR-2000; 2000WO-US06280.  
 PF  
 XX 09-MAR-1999; 99US-0123667.  
 PR 08-MAR-2000; 2000US-0123667.  
 PR  
 XX (CURA-) CURAGEN CORP.  
 PA  
 XX Shimkels RA;  
 PI  
 XX WPI: 2000-594318/56.  
 DR P-PSDB; AAB23033.  
 DR  
 XX Novel human membrane associated or secreted polypeptides and  
 PT polynucleotides useful for diagnosis, prevention and treatment of  
 PT pathological states such as cancer, immune, cardiovascular and  
 PT neurological disorders -  
 PT  
 XX Claim 3; Fig 5; 151PP; English.  
 PS  
 XX Sequences AAA93616-A93631 and AAA93673-A93676 represent nucleic acids  
 CC which encode human SECX proteins (AAB23029-823048). The SECX proteins  
 CC of the invention are either secreted or membrane-associated proteins  
 CC and act as regulator of cellular proliferation and differentiation. SECX  
 CC proteins or nucleotides are useful for diagnosing the presence of, or  
 CC predisposition to, a disease associated with altered levels of SECX  
 CC proteins and nucleotides. The SECX proteins are also useful to screen  
 CC compounds that modulate SECX activity or expression. The interaction of  
 CC a SECX protein with other cellular proteins may be useful to modulate  
 CC the activity of a partner protein, cellular proliferation, cellular  
 CC differentiation and cell survival. SECX nucleotides are useful for the  
 CC recombinant expression of SECX protein, and may be used to detect SECX mRNA  
 CC or genetic lesions in the SECX gene. They may also be used to modulate  
 CC SECX expression (e.g., using antisense oligonucleotides). SECX nucleic  
 CC acid sequences are also useful for identifying a cell or tissue type in  
 CC a biological sample, and in forensic biology. SECX primers or probes are  
 CC useful for detecting the presence of SECX nucleotides and for screening  
 CC tissue cultures for contamination. Diseases that may be treated or  
 CC prevented using SECX proteins or nucleotides include cancer (e.g.,  
 CC colorectal carcinoma, prostate cancer), benign tumours, immune disorders  
 CC (including autoimmune diseases, transplant rejection, allergies, AIDS),  
 CC infections, inflammatory disorders, arthritis, haematopoietic disorders,  
 CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,  
 CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g.,  
 CC surgical or traumatic wounds, spinal cord injury), and skeletal  
 CC disorders.  
 XX  
 SQ Sequence 2341 BP, 565 A, 708 C, 565 G, 503 T, 0 other;  
 Alignment scores:  
 Pred. No.: 3,216-287 Length: 2341  
 Score: 3446.00 Matches: 653  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 21 Gaps: 0

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 QY 1 MetLysLeuLeuTPGInValThrValHisHisThrTrpAsnAlaIleLeuLeuPro 20  
 DB 215 ATGAAGCTCTTGCGCAGTAACTGACACACACCTGGAAATGCACTCTCTCCG 274  
 QY 21 PheValTyrLeuThrAlaGlnValTrpIleLeuCysAlaAlaIleAlaAlaSer 40  
 DB 275 TTGGTCACTCAAGCGGCGCAAGTGTGATCTGTGTGACAGCACTGGTGGCGGCTCA 334  
 QY 41 AlaGlyProGlnAsnCysProSerValCysSerCysSerArgGlnPheSerValVal 60  
 DB 335 GCCGGGCCCGCAAGACTCCCTCCGTGCTCGTCGAGTAACCACTGACAGAAAGTGTG 394  
 QY 61 CyeThrArgArgGlyLeuSerGlnValProGlnGlyIleProSerAsnThrArgTyrLeu 80  
 DB 395 TGCACGCGCGGGGCTCTCCGAGGTCCCGAGGGATTTCTTGAACACCGGGTACTCTC 454  
 QY 81 AsnLeuMetGluAsnAsnIleGlnMetIleGlnAlaAspThrPheArgHisLeuHis 100  
 DB 455 AACCTCATGGAGAAACAATCCAGATGATCCAGGCCGACACTTCCGCCACTCACAC 514  
 QY 101 LeuGlnValLeuGlnLeuGlyArgAsnSerIleArgGlnIleGlnValGlyAlaPheAsn 120  
 DB 515 CTGAGAGGTCTCGCAGTTGGCGAGAACTCCATCCGAGATGAGTGGGGGCTTCAAC 574  
 QY 121 GlyLeuAlaSerLeuSerThrLeuGlnLeuPheAspAsnTrpLeuThrValIleProSer 140  
 DB 575 GGCCTGGCCAGCTTCACACACCTGGAGCTGTTCACAACCTGGCTGACAGTCACTCAAGC 634  
 QY 141 GlyAlaPheGlnTyrLeuSerTyrLeuArgGlyLeuTrpLeuArgAsnProIleGln 160  
 DB 635 GGGGCTTTGAATACCTGTCCAACTCGGGAGCTCTGGCTTCCCAACAACCCATGGA 694  
 QY 161 SerIleProSerTyrAlaPheAsnArgValProSerLeuMetArgLeuAspLeuGlyGlu 180  
 DB 695 AGCATCCCTCTTACGCTTCAACCGGGGTCCCTCCATCGCCCTGAGCTGGGGAG 754  
 QY 181 LeuValTyrLeuGlnTyrIleSerGlnGlyAlaPheGlnGlyLeuPheAsnLeuTyr 200  
 DB 755 CTCAAGAGCTGGAGATATCTCGAGAGACTTTTGAAGGGGCTGTCAACTCAAGAT 814  
 QY 201 LeuAsnLeuGlnMetCysAsnIleLeuAspMetProAsnLeuThrProLeuValGlyLeu 220  
 DB 815 CTGAATCTGGGCACTGTCAACATTTAAAGACATGCCCAATCCACCCCTGTGGGCTG 874  
 QY 221 GlnGluLeuGlnMetSerGlyAsnHisPheProGlnIleArgProGlySerPheHisGly 240  
 DB 875 GAGGAGCTGGAGATGTCAAGGAAACCACTTCCCTGAGATCAAGGCTGCTCCATGGC 934  
 QY 241 LeuSerSerLeuValTyrLeuTrpValMetAsnSerGlnValSerLeuIleGlnArgAsn 260  
 DB 935 CTGAGCTCCCTCAAGAGACTCTGGGTATGTAACACAGGTCAGCTGATTTGACCGGAT 994  
 QY 261 AlaPheAspGlyLeuAlaSerLeuValGlyLeuAsnLeuAlaHisAsnAsnLeuSerSer 280  
 DB 995 GCTTTTACGGGCTGGCTTCACTTGTGAACTCAACTTGGCCCACTAACTCTCTTCT 1054  
 QY 281 LeuProHisAspLeuPheThrProLeuArgTyrLeuValGlyLeuHisLeuHisAsn 300  
 DB 1055 TTGGCCCATGACTCTTACCCCGCTGAGGTAACCTGGTGGAGTTGACTTACACACAAAC 1114  
 QY 301 ProTrpAsnCysAspCysAspIleLeuTrpLeuAlaTrpTrpLeuArgGlyTyrTyrLeu 320  
 DB 1115 CTTTGAACCTGTGATTTGATTTCTGTGGCTACCTGGTGGCTTTCAGAGATATATACCC 1174  
 QY 321 ThrAsnSerThrCysCysGlyArgCysHisAlaProMetHisMetCysArgGlyArgTyrLeu 340  
 DB 1175 ACCAATTCACCTCTGTGGCGGCTGTCACTCCATGACACAGCGAGCGGCTACTCTC 1234  
 QY 341 ValGlnValAspGlnAlaSerPheGlnCysSerAlaProPheIleMetAspAlaProArg 360



Db 1235 GTGAGGTGACGACGCTCTTCACTGCTCTGCCCCCTTCATCATGACGACCTCGA 1294  
 Qy AspleuansnilesSerGluGlyArgMetAlaGluLeuGlyCysArgThrProPmetSer 380  
 Db 1295 GACTCAACATTTTGAGGGGTGGATGGCACAATTAAGTTCGAGCTCCCCCTATGTC 1354  
 Qy SerVallystrPleuLeuProAsnGlyThrValLeuSerHisAlaSerArgHisProArg 400  
 Db 1355 TCCCTGAAGTGTGTGCTGCCAATGGGACAGTGTCTGACGACGCTCCCGCCCAAGG 1414  
 Qy 401 IleSerValLeuAsnArgGlyThrLeuAsnSerHisValLeuLeuSerAspThrGly 420  
 Db 1415 ATCTGTGCTCCCAACGACGACCTTGAACCTTTCCACGCGCTTCCTTGACACCTGGG 1474  
 Qy ValTyThrCysMetGlyThrAsnValAlaGlyAsnSerAsnAlaSerAlaTyLeuAsn 440  
 Db 1475 GTGACACATGACGAGGACCAATGTTGACGACCACTCCAGCTCGGCTTACTCAT 1534  
 Qy 441 GlySerThrAlaGluLeuAsnThrSerAsnTySerPhePheThrGlyThrGlyGlu 460  
 Db 1535 GGGAGCACGCTGAGCTTAAACCTCCCACTACAGCTTCTTACCAACAGGAGGAG 1594  
 Qy 461 ThrThrGluLeuSerProGluAspThrThrArgGlyTyLeuProValProThrThrSer 480  
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 Db 1655 ACTGGTATCCAGCCGGCATTAACACTCTTACACGCTGCTCATTCACACTACCCGATG 1714  
 Qy 501 ProlysglnValAlaValProAlaThrAspThrThrAspTyMetGlnThrSerLeuAsp 520  
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 Qy 541 AlaAlaMetIleValPheTyLeuLeuArgIleGlnIleArgSerThrVal 560  
 Db 1835 GCGCCCATGTTGATGCTTCTTATTAACCTTGTAAAGCGGACACGAGGAGTACAGTC 1894  
 Qy 561 ThrAlaAlaArgThrValGluIleIleGlnValAspGluAspIleProAlaAlaThrSer 580  
 Db 1895 ACAGCCCGCCGAGCTGTTGATATATCCAGGTGACAGACATCCAGACGACAACTCC 1954  
 Qy 581 AlaAlaAlaThrAlaAlaProSerGlyValSerGlyGluGlyAlaValLeuProThr 600  
 Db 1955 GCACGACCAACAGACGCTCCCGGTGTATCAGGTGAAGGGGACAGTGTCTCCCA 2014  
 Qy 601 IleHisAspHisIleAsnTyAsnThrTyLeuProAlaHisGlyAlaHisIleThrThrGlu 620  
 Db 2015 ATTATGATCATTAATTAATCAACACCTCAACACAGACATGGGGCCCACTGACAGAA 2074  
 Qy 621 AsnSerLeuGlyAsnSerLeuHisIleProThrValThrThrIleSerGluProTyIleIle 640  
 Db 2075 AACAGCCTGGGGAATCTCTGCAACCCCACTACCACTACTGAACTTATTAATT 2134  
 Qy 641 GlnThrHisThrIleAspGlyValGlnGluThrGlnIle 653  
 Db 2135 CAGACCATATCCAGAGCAAGTACAGAGAACTCAATAA 2173  
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 AC AAD16345;  
 XX 19-NOV-2001 (first entry)  
 DT  
 XX Human sbgPRO331a gene.  
 DE Human sbgPRO331a gene.  
 XX Human, Alzheimer's disease; amyotrophic lateral sclerosis;

KM ALS; Zollinger-Ellison syndrome; immune system disease; schizophrenia;  
 KM inflammation; haematopoietic disease; anxiety; feeding disorder; aging;  
 KM anorexia; depression; cardiovascular disease; sleep disorder; seizure;  
 KM memory alteration; migraine; stroke; asthma; neuropathy; hypoglycaemia;  
 KM sexual disorder; growth abnormality; infection; autoimmune disease;  
 KM rheumatoid arthritis; cataractogenesis; angiogenesis; atherosclerosis;  
 KM cerebral ischaemia; cirrhosis; Huntington's disease; Hodgson's disease;  
 KM hypercholesterolaemia; headache; amnesia; cardiac arrhythmia; obesity;  
 KM diabetes mellitus; glomerulonephritis; renovascular hypertension;  
 KM cancer; vaccine; gene therapy; sbgPRO331a gene; ds.  
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 XX  
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 FT CDS 1..1962  
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 FT /product= "Human sbgPRO331a protein"  
 XX  
 PN W0200160850-A1.  
 XX  
 PD 23-AUG-2001.  
 XX  
 PE 14-FEB-2001; 2001WO-US04703.  
 XX  
 PR 14-FEB-2000; 2000US-0182172.  
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 PR 29-FEB-2000; 2000US-0186084.  
 XX  
 PR 18-APR-2000; 2000US-0198583.  
 XX  
 PR 04-OCT-2000; 2000US-0237963.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Agrawal P, Kabnick KS, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;  
 XX  
 DR WPI; 2001-536566/59.  
 XX  
 DR P-PSDB; AAE09438.  
 XX  
 PT New secreted and membrane associated polypeptides for treating  
 PT Alzheimer's disease, peoriasis, cancer, enterocolitis, sleep and sexual  
 PT disorders, stroke, and asthma -  
 XX  
 PS Claim 2; Page 37-38; 94pp; English.  
 XX  
 CC The present sequence is a gene encoding human sbgPRO331a protein,  
 CC a membrane bound protein of the invention.  
 CC The invention relates to secreted and membrane associated polypeptides  
 CC and nucleic acid molecules encoding such polypeptides. Sequences of the  
 CC invention are useful for treating diseases such as Alzheimer's disease,  
 CC amyotrophic lateral sclerosis (ALS), Zollinger-Ellison syndrome, diseases  
 CC of the immune system, haematopoietic disease, inflammation, anxiety,  
 CC schizophrenia, feeding disorders, anorexia, depression, social, sexual  
 CC and rewarded behaviour, cardiovascular disease, sleep disorder, learning  
 CC and memory alteration and altered immune response, seizure, migraine,  
 CC cancer, stroke, asthma, neuropathy, aging, sexual disorders, treatment  
 CC of transsexuals, growth abnormalities, obesity, infections, autoimmune  
 CC diseases (e.g. rheumatoid arthritis), cataractogenesis, angiogenesis,  
 CC disorders associated with healthy maintenance of gastric mucosa and  
 CC repair of acute and chronic mucosal lesion, lung carcinoma, cerebral  
 CC ischaemia, atherosclerosis, cirrhosis, Huntington's disease, headache,  
 CC amnesia, multiple sclerosis, Hodgson's disease, dilated cardiomyopathy,  
 CC congestive heart failure, cardiac arrhythmias, hypercholesterolaemia,  
 CC viral and non-viral hepatitis, type I and type II diabetes mellitus,  
 CC glomerulonephritis, renovascular hypertension, hypoglycaemia, periodic  
 CC paralysis, tendinitis and malignant hyperthermia. Polypeptides of the  
 CC invention are used to identify membrane bound and soluble receptors.  
 CC They are also useful as vaccines for inducing an immunological response  
 CC in a mammal. Polynucleotides of the invention are used in gene therapy.  
 CC They are also valuable for chromosome localisation studies and tissue  
 CC expression studies.  
 XX  
 SQ Sequence 1962 BP; 444 A; 622 C; 482 G; 414 T; 0 other;  
 Alignment Scores:

Pred. No.: 5,78e-284 Length: 1962  
 Score: 3407.00 Matches: 648  
 Percent Similarity: 99.39% Conservative: 1  
 Best Local Similarity: 99.23% Mismatches: 4  
 Query Match: 98.87% Indels: 0  
 DB: 22 Gaps: 0

US-09-991-053-10 (1-653) x AAD16345 (1-1962)

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 Db 1 ATGAGCTCTTGTGCGAGTAACTGTGACACCAACCTGGATGCCATCTGCTCCG 60  
 QY 21 PheValTyrLeuThrAlaGlnValTrrPLeuCySaAlaAlaIleAlaAlaSer 40  
 Db 61 TTGCTTAACCTCAGCGGCGCAAGTGTGATCTGTGTGACGACATCGTGTGCGGCTCA 120  
 QY 41 AlaGlyProGlnAsnCyProSerValCysSerCysSerAsnGlnPheSerLysValVal 60  
 Db 121 GCCGGGCCCCAGAACTGCCCTCCCTGCTGTGCTGCAATAACAGTTCAGCAAGGTGTG 180  
 QY 61 CysThrArgArgGlyLeuSerGluValProGlnGlyIleProSerAsnThrArgTyrLeu 80  
 Db 181 TGCACGGCGCGGCTCTCCGAGGTCCCGAGGGATATCCCTCGAACACCGGTAACCTC 240  
 QY 81 AsnLeuMetGluAsnAsnIleGlnMetIleGlnAlaAspThrPheArgHisLeuHisHis 100  
 Db 241 AACCTCATGGAACAACATCATCATGATGCCAGCGCCACACTTCCGCACTCCACACAC 300  
 QY 101 LeuGluValLeuGlnLeuGlyArgAsnSerIleArgGlnIleGluValAlaPheAsn 120  
 Db 301 CTGAGAGCTCTGCAAGTGTGGCAGAACTCCATCCGCGAGATTGAGTGGGGCTTCAC 360  
 QY 121 GlyLeuAlaSerLeuSerThrLeuGlnLeuPheAsnProLeuThrValIleProSer 140  
 Db 361 GGCCGTGGCAGCTCAACACCTGGAGCTGTTCGACACTGCTGACGATCCCTAGC 420  
 QY 141 GlyAlaPheGluTyrLeuSerLysLeuArgGluLeuTrrPLeuArgAsnAsnProIleGlu 160  
 Db 421 GGGGCTTTGAATACCTGTCCAGCTGGGAGCTGTGGCTTCGGAACAACCCATCGAA 480  
 QY 161 SerIleProSerTyrAlaPheAsnArgValProSerLeuMetArgLeuAspLeuGlyLeu 180  
 Db 481 AGCATCCCTCTTACGCTTCAACCGGGGTGCCCTCCCTCATGCGCTGAGACTTGGGGAG 540  
 QY 181 LeuValysLeuGluTyrIleSerGlnGlyAlaPheGluGlyLeuPheAsnLeuLysTyr 200  
 Db 541 CTCAAGAGCTGGAGTATATCTGAGGGAGCTTTTGAAGGGCTGTTCACCTCAAGTAT 600  
 QY 201 LeuAsnLeuGlyMetCysAsnIleLysAspMetProAsnLeuThrProLeuValGlyLeu 220  
 Db 601 CTGAACCTTGGGCAATGTGCAACATTAAAGACATGCCCAATCTCACCCCTGTGGGGCTG 660  
 QY 221 GlnGluLeuGlnMetSerGlyAsnHisPheProGluIleArgProGlySerPheHisGly 240  
 Db 661 GAGAGCTGGAGATGTCAAGGAAACCACTTCCCTGAGATCAAGCGCTGCTTCATGTC 720  
 QY 241 LeuSerSerLeuLysLeuLeuTrrValMetAsnSerGlnValSerLeuIleGluArgAsn 260  
 Db 721 CTGAGCTCCCTCAAGAACCTCTGGGTCAATGAACTCAAGGTCAAGCTCAATGAGGGAGAT 780  
 QY 261 AlaPheAspGlyLeuAlaSerLeuValGluLeuAsnLeuAlaHisAsnAsnLeuSerSer 280  
 Db 781 GCTTTGACGGGCTGGCTTCACTGTGTGAACCTCAACTTGGCCCAACAAATACCTCTTCT 840  
 QY 281 LeuProHisAspLeuPheThrProLeuArgTyrLeuValGluLeuHisLeuHisAsn 300  
 Db 841 TTGCCCATGACCTCTTAACCCCGCTGAGGTACCTGGTGGAGTTGCACTACACACAC 900  
 QY 301 ProTrrPancCyAspCyAspIleLeuTrrPLeuAlaTrrTrrPLeuArgGluTyrIlePro 320  
 Db 901 CTTTGAACCTGTGATTGTGACATCTGTGGCTAGGCTGTGGCTTGCAGAGTATATACCC 960

QY 321 ThrAsnSerThrCysCyGlyArgCysHisAlaProMetHisMetArgGlyArgTyrLeu 340  
 Db 961 ACCAATTCACCTGCTGTGGCCGCTGTGATGCTCCCATGACATGACAGGCGGCTTACCTC 1020  
 QY 341 ValGluValAspGlnAlaSerPheGlnCysSerAlaProPheIleMetAsnAlaProArg 360  
 Db 1021 GTGAGGTGTGACAGGCTCTCTTCAAGTGTCTGCCCCCTTCATCAATGACAGCACTTGA 1080  
 QY 361 AspLeuAsnIleSerGlnGlyArgMetAlaGluLeuLysCysArgTrpProPheMetSer 380  
 Db 1081 GACTCAACATTTCTGAGGGTCCGATGCGAGAACTTAAGTGTGGAATCTCCCATATGTC 1140  
 QY 381 SerValIysTrrPLeuLeuProAsnGlyThrValLeuSerHisAlaSerArgHisProArg 400  
 Db 1141 TCCGTGAAGTGTGTGCTGCCCAATGGGACAGTGTCCAGCAAGCTCCCGCAACCAAG 1200  
 QY 401 IleSerValLeuAsnAspGlyThrLeuAsnPheSerHisValLeuLeuSerAspThrGly 420  
 Db 1201 ATCTGTGTCTCAACGAGGACCTTGAACCTTTCCACGCTGTCTTTCAGACACTGGG 1260  
 QY 421 ValTyrThrCysMetGlyThrAsnValAlaGlyAsnSerAsnAlaSerAlaTyrLeuAsn 440  
 Db 1261 GTGTACACATGATGATGACCAATGTTGACAGCACTCCAGCTGCTGCTTACTCAAT 1320  
 QY 441 GlySerThrAlaGluLeuAsnThrSerAsnTyrSerPhePheThrArgIleGlyLeu 460  
 Db 1321 GTGAGCAGCGGTGATTAACCTCACTCAAGCTTCTTACCAACAGTAAACAGTGGAG 1380  
 QY 461 ThrThrGluIleSerProGluAspThrThrArgLysTyrLysProValProThrThrSer 480  
 Db 1381 ACCACGAGATCTCTGCTGTGAGGACAAACGGAAGTAAACAGCTGTCTTCAACACATCC 1440  
 QY 481 ThrGlyTyrGlnProAlaTyrThrThrSerThrThrValLeuIleGlnThrThrArgVal 500  
 Db 1441 ACTGTTACACAGCCGCGATATACCACTTACCAAGTGTCTTCACTTCACTTCACTGCTG 1500  
 QY 501 ProLysGlnValAlaValProAlaThrAspThrThrAspLysMetGlnThrSerLeuAsp 520  
 Db 1501 CCCAAGCAGGTGGAGTACCGCGGACAGACCACTGACAAAGATGACAGACAGCTGGAT 1560  
 QY 521 GluValMetLysThrThrLysIleIleIleGlyCysPheValAlaValThrLeuLeuAla 540  
 Db 1561 GAACTCATGAAAGCACCAAGATCATATGCTGTGTGGTGTGGAGTGAATCTGTAGCT 1620  
 QY 541 AlaAlaMetLeuIleValPheTyrLysLeuArgLysArgHisGlnGlnArgSerThrVal 560  
 Db 1621 GCCGCCATGTGATGTCTTCTTAACTTCTGTAAGCGGACACGACGCGGAGTACATC 1680  
 QY 561 ThrAlaAlaArgThrValGluIleIleGlnValAspGluAspIleProAlaAlaThrSer 580  
 Db 1681 ACAGCCCGCGGACTGTGTGATATATCCAGGTGACGAGACATCCAGACGAAATCC 1740  
 QY 581 AlaAlaAlaThrAlaAlaProSerGlyValSerGlyGluGlyAlaValValLeuProThr 600  
 Db 1741 GCACACACAAACAGAGCTCCGCTCGGTATCAAGTGAAGGGGAGTGAAGTGTCCCA 1800  
 QY 601 IleHisAspHisIleAsnTyrAsnThrTyrLysProAlaHisGlyAlaHisIleProThrGlu 620  
 Db 1801 ATTATATACCAATATTAATCAACACCTACAAACACAGCACTGGGGCCCATGTGAAGAA 1860  
 QY 621 AsnSerLeuGlyAsnSerLeuHisProThrValThrThrIleSerGluProTyrIle 640  
 Db 1861 AACAGCTGGGGAATCTGTGACCCCAACAGTCAACATCTTGAACCTTATATAT 1920  
 QY 641 GlnThrHisThrLysAspLysValGlnGluThrGlnIle 653  
 Db 1921 CAGACCATATCAAGGACAAAGTACAGAAATCAATA 1959

RESULT 3  
 AAC58383  
 ID AAC58383 standard; cDNA; 2185 BP.  
 XX  
 AC AAC58383;

XX 29-JAN-2001 (first entry)  
 XX Best Local Similarity: 99.39%  
 XX Query Match: 98.87%  
 XX DB: 21

Human PRO1111 nucleotide sequence SEQ ID NO:45.  
 Human: tumour; diagnosis; neoplastic disease; neoplastic cell growth;  
 proliferation; tumorigenesis; identification; cancer; cytostatic;  
 neurotrophic; neuroprotective; antiinflammatory; immunosuppressive;  
 immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;  
 neuronal disorder; glial disorder; astrocytoma; angiogenic;  
 hypochalamic disorder; glandular disorder; macropthal disorder;  
 epithelial disorder; ectomal disorder; blastocoele disorder;  
 inflammatory disorder; immunologic disorder; ss.

XX Homo sapiens.  
 XX NO200053755-A2.  
 XX 14-SEP-2000.  
 XX 06-JAN-2000; 2000WO-US00376.

XX 08-MAR-1999; 99WO-US05028.  
 XX 02-JUN-1999; 99WO-US12252.  
 XX 23-JUN-1999; 99US-0141037.  
 XX 07-JUL-1999; 99US-0143048.  
 XX 26-JUL-1999; 99US-0145698.  
 XX 30-NOV-1999; 99WO-US28313.  
 XX 20-DEC-1999; 99WO-US30911.  
 XX 05-JAN-2000; 2000WO-US00219.

XX (GETH ) GENENTECH INC.  
 XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;  
 XX Metanabe CK, Wood WI;  
 XX WPI; 2000-572270/53.  
 XX P-PSDB; AAB24073.

XX Thirty PRO polynucleotides encoding PRO polypeptides, useful in the  
 XX treatment, diagnosis and prevention of cancer -  
 XX Claim 50; Fig 33; 286pp; English.

XX The present invention describes an isolated antibody that binds to  
 XX one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO355,  
 XX PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,  
 XX PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,  
 XX PRO1187, PRO1281, PRO1293, PRO1304, PRO1317, PRO1710, PRO2094,  
 XX PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell  
 XX growth. The PRO polypeptides and nucleotides are useful in the  
 XX treatment, diagnosis and prevention of cancer. The antibodies and other  
 XX anti-tumour compounds may be used to treat various conditions, including  
 XX those characterised by overexpression and/or activation of the amplified  
 XX PRO genes. Exemplary conditions or disorders to be treated with such  
 XX antibodies and other compounds include benign or malignant tumours  
 XX (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,  
 XX colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic  
 XX carcinomas, sarcomas, glioblastomas, and various head and neck tumours),  
 XX leukemias and lymphoid malignancies, other disorders such as neuronal,  
 XX glial, astrocytoma, hypochalamic and other glandular, macropthal,  
 XX epithelial, stromal and blastocoele disorders, and inflammatory,  
 XX angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR  
 XX primers and hybridisation probes used in the isolation of the human PRO  
 XX sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human  
 XX PRO polynucleotide and protein sequences given in the exemplification of  
 XX the present invention.

XX Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;

Alignment Scores: 6.73e-284 Length: 2185  
 Pred. No.: 3407.00 Matches: 648  
 Score:

Percent Similarity: 99.39%  
 Best Local Similarity: 99.23%  
 Query Match: 98.87%  
 DB: 21

Conservative: 1  
 Mismatches: 4  
 Indels: 0  
 Gaps: 0

US-09-991-053-10 (1-653) x AAC58383 (1-2185)

Qy 1 MetLysLeuLeuTPGInVAlITThrValH:SHiSHiThrTPraAnaIaIeLeuPro 20  
 Db 57 ATGAAGCTCTTGGAGGAGTACTGTGCACACCACTGGATGCCATCTCTCCG 116  
 Qy 21 PheValTyrLeuThrAlaGlnValITrpIleLeuCysAlaIaIaIaIaIaIaSer 40  
 Db 117 TTGCTTACCTCAACGGGCAAGTGTGATCTGTGTGCACGATCGTGTGGCGCTCA 176  
 Qy 41 AlaGlyProGlnAnCySPSerValCysSerCysSerAnGlnPheSerLysVal 60  
 Db 177 GCCGGGCCCGAAGACTGCCCTCCGTTGCTGTCAGTAACCAAGTTCAGCAAGTGTG 236  
 Qy 61 CyethrArgArgGlyLeuSerGluValProGlnGlyIleProSerAnThrArgTyrLeu 80  
 Db 237 TGCAAGCGCGGAGCTCTCCAGAGTCCGAGGATATCCCTTGAACACCGGATACCTC 296  
 Qy 81 AsnLeuMetGluAnAsnIleGlnMetIleGlnAlaSerThrPheArgHis 100  
 Db 297 AACCTATGAGAAACAACATCCAGATATCCAGGCGCAACCTTCCGCCACTCCACAC 356  
 Qy 101 LeuGluValLeuGlnLeuGlyArgAnSerITleArgGlnIleGluValGlyAlaPheAsn 120  
 Db 357 CTGAGGCTCTTGACGTTGGGAGGAGCAATCCATCCGAGATGAGTGGGGGCTTCAC 416  
 Qy 121 GlyLeuAlaSerLeuSerThrLeuGlnLeuPheAspAnThrPheValIleProSer 140  
 Db 417 GGCTTGCCAGCTTCAACACCTCGAGCTGTGCAACCTGGCTGAGAGTATCTTACG 476  
 Qy 141 GlyAlaPheGluTyrLeuSerTyrLeuArgGluLeuTrpLeuArgAnAsnProIleGlu 160  
 Db 477 GGAGCTTTGAATACCTGTCACAGCTCGGAGAGTCTGGCTTGCAACCAACCCATGAA 536  
 Qy 161 SerIleProSerTyrAlaPheAnArgValProSerLeuMetArgLeuAspLeuGlyGlu 180  
 Db 537 AGCATCCCTCTTAAGCTTCAACCGGAGTCCCTCTCATGCGCTGAGCTGGGGAG 596  
 Qy 181 LeuLysLeuGlnTyrTrpIleSerGluGlyAlaPheGluLeuPheAnLeuLysTyr 200  
 Db 597 CTCAAGAGCTGAGATATCTCTGAGAGGCTTTGAGAGGCTGTTCAACCTCAAGTAT 656  
 Qy 201 LeuAnLeuGlyMetCysAnIleLysAspMetProAnLeuThrProLeuValGlyLeu 220  
 Db 657 CTGAACCTGGGCAATGTCAACATTAAGAATGCCCAATCTCACCCCTGTGGGCTG 716  
 Qy 221 GlnGluLeuGlnMetSerGlyAnHisPheProGluIleArgProGlySerPheHisGly 240  
 Db 717 GAGAGCTGAGATGTGAGGAGCAACCTTCTGAGATGAGGCTGCTCTTCATGGC 776  
 Qy 241 LeuSerSerLeuLysLeuTrpValMetAnSerGlnValSerLeuIleGluArgAsn 260  
 Db 777 CTGAGCTCCCTCAAGAGCTCTGGTCAATGAACCAAGGTGACCTGATTGACCGAAT 836  
 Qy 261 AlaPheAspGlyLeuAlaSerLeuValGlnLeuAnLeuAlaHisAnAnLeuSerSer 280  
 Db 837 GCTTTTACCGGCGGCTTCACTTGTGAATCACTGAGCACTGGCCCAATTAACCTCTTCT 896  
 Qy 281 LeuProHisAspLeuPheThrProLeuArgTyrLeuValGlnLeuHisHisAsn 300  
 Db 897 TTGGCCCATGACCTTACCCGCTGAGGATACCTGTGAGATGATCAACACCAAC 956  
 Qy 301 ProTrpAnCyAspProCysAspIleLeuTrpLeuAlaITrpTrpLeuArgGlyTyrIlePro 320  
 Db 957 CCTTGAACTGTATGTGACATTTGTGGCTGCTGAGCTTCAAGAGTATATACCC 1016  
 Qy 321 ThrAnSerThrCysCysGlyArgCysHisAlaProMetHisMetArgGlyArgTyrLeu 340

Db 1017 ACCAATTCACCTGCTGTGGCCGCTGTCATAGTCTCCATGACATGCGAGCCGCTACTC 1016  
Qy 341 ValGluValAspGlnAlaSerPheGlnCysSerAlaProPheIleMetAspAlaProArg 360  
Db 1077 GTGAGAGGAGACAGCCCTCTTCCAGTGTCTGTGCCCCCTTCATCATGAGACGCACTGGA 1156  
Qy 361 AspleuAnlIleSerGluGlyArgMetAlaGluLeuLysCysArgThrProPrometSer 380  
Db 1137 GACCTCAACATTTCTGAGGGTGTGGATGGCAGAACTTAATGTGCGACTCCCTATGTCC 1196  
Qy 381 SerValIleThrPleuLeuProAnGlyThrValIleuSerHisAlaSerArgHisProArg 400  
Db 1197 TCCGTAAGTGTGTCTGCTCCCATAGGACAGTGTCCACCGCTCCCGCCACCAAGG 1256  
Qy 401 ILeSerValIleuAsnAspGlyThrIleuAnPheSerHisValIleuLeuSerAspThrGly 420  
Db 1257 ATCTGTCTCTCAAGACGCGACTTGAACCTTTCCACGTCTCTTTCAGACACTGG 1316  
Qy 421 ValIYrThrCysMetGlyThrAsnValAlaGlyAsnSerAsnAlaSerAlaIYrIleuAn 440  
Db 1317 GTGTACATCATGTCATGACCAATGTTCAGGCACTCCAAAGCTCGGCTACTCAAT 1376  
Qy 441 GlySerThrAlaGluLeuAnThrSerAnTYrSerPhePheThrThrGlyThrGlyGlu 460  
Db 1377 GTGACACGGCTGAGCTTAACCTTCACTCAACAGCTTCTTCCACAGTACAGTGGAG 1436  
Qy 461 ThrThrGluIleSerProGluAspThrThrArgIleYrIYrLysProValProThrThrSer 480  
Db 1437 ACCACGGAGATCTGCTGAGGACACAAAGCGAAAGTACAAAGCTGTCTTCCACCGTCC 1496  
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Db 1497 ACTGGTACACAGCCGCGATATACCACTCACTCAACAGGTGCTCATTCAGACTACCGGTG 1556  
Qy 501 ProIYrGlnValAlaValProAlaThrAspThrThrArgIleYrIleuSerThrSer 520  
Db 1557 CCCAAGCAGGTGGAGTACCCCGCAGACACACACTGACAAAGATGACAGCCAGCTGAT 1616  
Qy 521 GluValIleLysThrThrIleIleIleGlyCysPheValAlaValThrIleuLeuAla 540  
Db 1617 GAAATCAGAAAGACCAACCAAGTATCATTTGGCTCTTGTGGCGATGACTGTGTAAGT 1676  
Qy 541 AlaAlaMetLeuIleValPheIYrIleuArgIleYrArgHisGlnGlnArgSerThrVal 560  
Db 1677 GCCCGCATGTGATGTCTTCTTAATACTTGTGTAAGCGGACACGAGCGAGTACAGTC 1736  
Qy 561 ThrIleAlaIleArgThrValGluIleIleGlnValAspGluAspIleProAlaAlaThrSer 580  
Db 1737 ACAGCCGCCGAGCTGTGAGTAAATCCAGGTGACGAAAGCATCCAGCGACCAATCC 1796  
Qy 581 AlaAlaIleThrAlaAlaProSerGlyValSerGlyGluGlyAlaValValIleuProThr 600  
Db 1797 GCAGACGACACAGCTCCGTCGGGTATCAGGTGAGGGGCGATGTGCTGCCACA 1856  
Qy 601 ILeHisAspHisIleAsnTYrAsnThrTYrIYrLysProAlaHisGlyAlaHisIleProThrGlu 620  
Db 1857 AFTCATGACCAATTAATTAACAACACCTAACAAACAGACACANTGGGCCACGTCGACAA 1916  
Qy 621 AsnSerLeuGlyAsnSerLeuHisProThrValIleThrIleSerGluProTYrIleIle 640  
Db 1917 AACACCCCTGGGAGACTTCTCTGACCCCAAGCACACACTATCTGAACTTATTAATTT 1976  
Qy 641 GlnThrHisIleThrIleAspIleValGlnIleuThrGlnIle 653  
Db 1977 CAGACCATACCAAGACAAAGTACAGAACTCAATA 2015

XX XX Membrane-bound protein PRO1111 encoding cDNA.  
DE Membrane-bound polypeptide: PRO polypeptide; LDL receptor; TIE ligand;  
XX pharaceutical; receptor immunoadhesin; gene mapping; sr.  
KW Homo sapiens.  
XX MO9963088-A2.  
XX PD 09-DEC-1999.  
XX PF 02-JUN-1999; 99WO-US12252.  
XX 02-JUN-1998; 98US-0087607.  
PR 02-JUN-1998; 98US-0087609.  
PR 02-JUN-1998; 98US-0087759.  
PR 03-JUN-1998; 98US-0087827.  
PR 04-JUN-1998; 98US-0088021.  
PR 04-JUN-1998; 98US-0088025.  
PR 04-JUN-1998; 98US-0088028.  
PR 04-JUN-1998; 98US-0088029.  
PR 04-JUN-1998; 98US-0088030.  
PR 04-JUN-1998; 98US-0088033.  
PR 04-JUN-1998; 98US-0088326.  
PR 05-JUN-1998; 98US-0088167.  
PR 05-JUN-1998; 98US-0088202.  
PR 05-JUN-1998; 98US-0088212.  
PR 05-JUN-1998; 98US-0088217.  
PR 05-JUN-1998; 98US-0088655.  
PR 10-JUN-1998; 98US-0088722.  
PR 10-JUN-1998; 98US-0088730.  
PR 10-JUN-1998; 98US-0088734.  
PR 10-JUN-1998; 98US-0088738.  
PR 10-JUN-1998; 98US-0088740.  
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PR 10-JUN-1998; 98US-0088810.  
PR 10-JUN-1998; 98US-0088811.  
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PR 11-JUN-1998; 98US-0088876.  
PR 12-JUN-1998; 98US-0089030.  
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PR 18-JUN-1998; 98US-0089801.  
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PR 18-JUN-1998; 98US-0089908.  
PR 19-JUN-1998; 98US-0089947.  
PR 19-JUN-1998; 98US-0089948.  
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PR 22-JUN-1998; 98US-0090252.  
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PR 23-JUN-1998; 98US-0090349.  
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PR 24-JUN-1998; 98US-0090435.  
PR 24-JUN-1998; 98US-0090444.  
PR 24-JUN-1998; 98US-0090445.

PR 24-JUN-1998; 98US-0090461.  
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 PR 24-JUN-1998; 98US-0090535.  
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 PR 24-JUN-1998; 98US-0090540.  
 PR 24-JUN-1998; 98US-0090557.  
 PR 25-JUN-1998; 98US-0090676.  
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 PR 25-JUN-1998; 98US-0090690.  
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 PR 25-JUN-1998; 98US-0090695.  
 PR 26-JUN-1998; 98US-0090696.  
 PR 26-JUN-1998; 98US-0090697.  
 PR 01-JUL-1998; 98US-0091358.  
 PR 01-JUL-1998; 98US-0091360.  
 PR 01-JUL-1998; 98US-0091544.  
 PR 02-JUL-1998; 98US-0091478.  
 PR 02-JUL-1998; 98US-0091486.  
 PR 02-JUL-1998; 98US-0091519.  
 PR 02-JUL-1998; 98US-0091626.  
 PR 02-JUL-1998; 98US-0091628.  
 PR 02-JUL-1998; 98US-0091633.  
 PR 02-JUL-1998; 98US-0091646.  
 PR 02-JUL-1998; 98US-0091673.  
 PR 07-JUL-1998; 98US-0091978.  
 PR 09-JUL-1998; 98US-0092182.  
 PR 10-JUL-1998; 98US-0092472.  
 PR 20-JUL-1998; 98US-0093339.  
 PR 30-JUL-1998; 98US-0094651.  
 PR 04-AUG-1998; 98US-0095282.  
 PR 04-AUG-1998; 98US-0095285.  
 PR 04-AUG-1998; 98US-0095301.  
 PR 04-AUG-1998; 98US-0095302.  
 PR 04-AUG-1998; 98US-0095318.  
 PR 04-AUG-1998; 98US-0095321.  
 PR 04-AUG-1998; 98US-0095325.  
 PR 10-AUG-1998; 98US-0095916.  
 PR 10-AUG-1998; 98US-0095929.  
 PR 10-AUG-1998; 98US-0096012.  
 PR 11-AUG-1998; 98US-0096143.  
 PR 11-AUG-1998; 98US-0096146.  
 PR 12-AUG-1998; 98US-0096329.  
 PR 17-AUG-1998; 98US-0096757.  
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 PR 18-AUG-1998; 98US-0096949.  
 PR 18-AUG-1998; 98US-0096950.  
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 PR 18-AUG-1998; 98US-0096960.  
 PR 18-AUG-1998; 98US-0097022.  
 PR 19-AUG-1998; 98US-0097141.  
 PR 20-AUG-1998; 98US-0097218.  
 PR 24-AUG-1998; 98US-0097661.  
 PR 26-AUG-1998; 98US-0097951.  
 PR 26-AUG-1998; 98US-0097952.  
 PR 26-AUG-1998; 98US-0097954.  
 PR 26-AUG-1998; 98US-0097955.  
 PR 26-AUG-1998; 98US-0097971.  
 PR 26-AUG-1998; 98US-0097974.  
 PR 26-AUG-1998; 98US-0097978.  
 PR 26-AUG-1998; 98US-0097979.  
 PR 26-AUG-1998; 98US-0097986.

PR 26-AUG-1998; 98US-0098014.  
 PR 31-AUG-1998; 98US-0098525.  
 PR 16-SEP-1998; 98US-0100634.  
 PR 12-JAN-1999; 99US-0115565.  
 XX (GERTH ) GENENTECH INC.  
 XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
 PI Wood WI, Yuan J;  
 XX WPI, 2000-072883/06.  
 DR P-PSDB; AAY6694.  
 XX Membrane-bound proteins and related nucleotide sequences -  
 PS Claim 2; Fig 156; 822pp; English.  
 XX The invention provides membrane-bound PRO polypeptides and  
 CC polynucleotides encoding them. The PRO sequences of the invention were  
 CC identified based on extracellular domain homology screening. The PRO  
 CC sequences have homology with proteins including LDL receptors, TIR  
 CC ligands and various enzymes. The membrane-bound proteins and receptor  
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
 CC immunoadhesins, for instance, can be used as therapeutic agents to block  
 CC receptor-ligand interactions. The membrane-bound proteins can also be  
 CC employed for screening of potential peptide or small molecule inhibitors  
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
 CC are useful as hybridization probes, in chromosome and gene mapping and in  
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences  
 CC will also be useful for the preparation of PRO polypeptides, especially  
 CC by recombinant techniques.  
 XX SO Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;

## Alignment Scores:

Pred. No.: 6,73e-284 Length: 2185  
 Score: 3407.00 Matches: 648  
 Percent Similarity: 99.39% Conservative: 1  
 Best Local Similarity: 99.23% Mismatches: 4  
 Query Match: 98.87% Indels: 0  
 DB: 21 Gaps: 0

US-09-991-053-10 (1-653) x AAZ65033 (1-2185)

QY 1 MetLysLeuLeuTPGInValIThrValHisHisHisThrTPAAnaIleLeuPro 20  
 DB 57 ATGAAGCTCTTGCGAGGTGAAGTGCACACACCTGGATGCACTGCTCCG 116  
 QY 21 PheValTyrLeuThrAlaGlnValITripIleLeuCyAlaIleAlaIleAlaSer 40  
 DB 117 TTGCTTAACTCAAGCGGCGAAGTGTGATTTCTGTGCAAGCATCGTGTGCGCTCA 176  
 QY 41 AlaGlyProGlnAnCyProSerValCySerCySerSerAnGlnPheSerValVal 60  
 DB 177 GCCGGGCCCAAGAACTGCCCTCGTTGCTCGAGTAACCAAGTTCAGCAAGTGTG 236  
 QY 61 CysThrArgArgGlyLeuSerGlnValIProGlnGlyIleProSerAnThrArgTyrLeu 80  
 DB 237 TGCACGGCGCGGCGCTCTCCAGAGTCCGCAAGGATTTCCCTGGAACACCCGGTACTC 296  
 QY 81 AsnLeuMetGluAnaAniIleGlnMetIleGlnAlaPheThrPheArgHisLeuHis 100  
 DB 297 AACCTCATGAGAAACAATCCAGATATCCAGGCCAACCTTCCGCCACTTCACAC 356  
 QY 101 LeuGluValIleuGlnIleuGlyArgAsnSerIleArgGlnIleGluValIleAlaPheAsn 120  
 DB 357 CTGAGGCTCTGCAAGTGGCGAAGAACTCCATCCGAGATTGAGTGGGGGCTTCAAC 416  
 QY 121 GlyLeuAlaSerLeuSerThrIleuGlnLeuPheAspAnThrPleuThrValIleProSer 140  
 DB 417 GGCCTGGCCAGCTTCACACCTGGAGCTGTTCACAACTGGCTGACAGATCATCCCTAGC 476  
 QY 141 GlyAlaPheGluTyrLeuSerTyrLeuArgGlnIleuThrPleuThrArgAnaAnProIleGlu 160

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Db      477 GGGGCGCTTTGAATACCTGTCAGAGTCGGAGAGCTGGCTTCCCAACACCCATCCAA 536
Qy      161 SerIleProSerTyrAlaPheAsnArgValProSerIleuMetArgLeuAspLeuGlu 180
Db      537 AGCATCCCTCTTACGCTTCAACCGAGTGCCTCCCTCATAGCGCTGGAATTGGGGAG 596
Qy      181 LeuIlyIleuLeuGluTyrIleSerGluValIlePheGluGluIleuPheAsnLeuIlyTyr 200
Db      597 CTCAAGAACTGAGATATATCTCTGAGGAGACTTTTGAAGGGCTGTCTCACTCAAGTAT 656
Qy      201 LeuAsnLeuGluMetCysAsnIleIlyAspMetProAsnLeuThrProLeuValGluIleu 220
Db      657 CTGAACCTGGGCACTGTGCACATTAAGACATGCCAATCTCACCCCTGTGGGGCTG 716
Qy      221 GluGluLeuGluMetSerGluYasnIlePheProGluIleArgProGluSerPheIleGlu 240
Db      717 GAGAGCTGGAGATCTCAGGAAACCATTCCTCTAGATCAGGCTGGCTCTTCCATGAC 776
Qy      241 LeuSerSerLeuIlyIleuTyrValMetAsnSerGluValSerLeuIleGluArgAsn 260
Db      777 CTGAGCTCCCTCAAGAACTCTGGGTCAATGAACTCAGAGTCAGCTGATTGAGGGAT 836
Qy      261 AlaPheAspGluLeuAlaSerIleuValGluLeuAsnLeuAlaIleAsnAsnLeuSer 280
Db      837 GCTTTGACGGGCTGGCTTCACTGTGGAACCTCACTGGCCCAATATACCTCTCTCT 896
Qy      281 LeuProIleAspLeuPheThrProLeuArgTyrIleuValGluLeuIleIleIleAsn 300
Db      897 TTGCCCCATGACCTTTTACCCCGCTGAGGTACTGGTGGAGTTGATCTTACACCAAC 956
Qy      301 ProTyrAsnCysAspCysAspIleuTyrPleuAlaTyrTyrPleuArgGluTyrIlePro 320
Db      957 CCTTGAACCTGATGTGATCTGTGAGCTGTGGCTGAGCTTGCAGAGATATATACC 1016
Qy      321 ThrAsnSerThrCysCysGluYargCysIleIlePheMetHisMetArgGluYargTyrIleu 340
Db      1017 ACCAATTCACCTGCTGTGGCGCGCTCATCTCCATGACATGCGAGCGCGCTACCTC 1076
Qy      341 ValGluValAspGluAlaSerPheGlnCysSerAlaPhePheIleMetAspAlaProArg 360
Db      1077 GTGAGGTGGACACGAGCTCTCTCCAGTGCCTGCCCCCTTCATATGAGACACCTGCA 1136
Qy      361 AspLeuAsnIleSerGluYargMetAlaGluLeuIlyCysArgThrProPheMetSer 380
Db      1137 GACCTCAACATTTCTGAGGTCGAGTGCAGAACTTAAGTGGCACTCCCTATATGTC 1196
Qy      381 SerValIlyTyrPleuLeuProAsnGluYthrValLeuSerHisIleSerArgHisProArg 400
Db      1197 TCCGTGAAGTGTGCTGCCCAATGGGACAGTGCACACCGCTCCCGCCACCAAG 1256
Qy      401 IleSerValIleAsnAspGluYthrIleuAsnPheSerHisValIleLeuSerAspThrGlu 420
Db      1257 ATCTCTGCTCTCAACGAGCGACCTTGAATTTTCCACGTGCTGCTTTCAGACACTGG 1316
Qy      421 ValTyrThrCysMetGluYthrAsnValAlaGluAsnSerAsnAlaSerAlaTyrIleuAsn 440
Db      1317 GTGTACATCATGATGATGACCAATGTTGACAGCACTCCACGCTCGGCTCACTCAT 1376
Qy      441 GlySerThrAlaGluLeuAsnThrSerAsnTyrSerPhePheIleThrGluIleGlu 460
Db      1377 GTGAGCAGCGCTGAGCTTAACCTCACTCAAGCTTCTTCAACACAGTAACTGAG 1436
Qy      461 ThrThrGluIleSerProGluAspThrThrArgIlyTyrIlyProValProThrThrSer 480
Db      1437 ACCACGGAGATCTCGCTGAGACCAACGCGAAAGTCAAGCCGTTCCTACACGCTCC 1496
Qy      481 ThrGluTyrGlnProAlaTyrThrThrSerThrThrValIleuIleGlnThrThrArgVal 500
Db      1497 ACTGTTTACGAGCGGCAATATACCACTCTACCAAGGTGCTCATTCACATCACTGCTG 1556
Qy      501 ProIySGlnValAlaValProAlaThrAspThrThrAspIlyMetGlnThrSerLeuAsp 520

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Db      1557 CCCAAGCAGGTGGCAGTACCCCGGACAGACCACTGACAGATGCAGACAGCTTGAT 1616
Qy      521 GluValMetIlyThrThrIlyIleIleGluCysPheValAlaValThrLeuLeuAla 540
Db      1617 GAATCATGAAAGACCAACGATATCATTTGGCTTTGTGGAGATCTGTAGCT 1676
Qy      541 AlaAlaMetLeuIleValPheTyrIlyLeuArgIlyValArgIleGlnIleArgSerThrVal 560
Db      1677 GCCGCCATGTGATGCTTCTTAATACTTCGTAAAGCGGACCAAGCAGGAGTACAGTC 1736
Qy      561 ThrIleAlaArgThrValGluIleIleGluValAspGluAspIleProAlaIleThrSer 580
Db      1737 ACACCCCGGAGCTGTGAGATATATCAGGTGACAGAGCATCCAGACAGCAATCC 1796
Qy      581 AlaAlaIleThrAlaIleAlaProSerGluValSerGluGluIlyAlaValIleuProThr 600
Db      1797 GCAGACCAACAGAGCTCCGTCGGTATCAGTAAAGGGGAGTATGCTGCCACA 1856
Qy      601 IleHisAspHisIleAsnTyrAsnThrTyrIlyProAlaHisIleTyrThrGlu 620
Db      1857 ATTCATGACCATATTAATCACTAACACCTACAAACACACATGGGCCCACTGGACAGAA 1916
Qy      621 AsnSerLeuGluYasnSerLeuHisProThrValThrIleSerGluProTyrIleIle 640
Db      1917 AACGCTGGGGAATCTCTGCACCCACAGTCCACTATCTGTGAACCTTATATATT 1976
Qy      641 GlnThrHisThrIlyAspIlyValGlnGluThrGlnIle 653
Db      1977 CAGACCATACCAAGGACAAAGTACAGAACTCAATA 2015

RESULT 5
AAS21462
ID AAS21462 standard; cDNA; 2185 BP.
XX
AC AAS21462;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human cDNA sequence encoding for PRO1111 polypeptide.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cathepsin; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW adipocyte; A-peptide; factor VIIa; gene therapy; ss.
XX
OS Homo sapiens.
XX
WC200140466-A2.
XX
PD 07-JUN-2001.
XX
PE 01-DEC-2000; 2000WO-US32678.
XX
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 09-DEC-1999; 99US-0170262.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31243.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 20-MAR-2000; 2000WO-US07377.

```

PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 10-NOV-2000; 2000WO-US30873.  
 XX  
 PA (GENTH ) GENENTECH INC.  
 XX  
 PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W,  
 PI Gerltsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI; 2001-408281/43.  
 P-PSDB; AAU12390.  
 XX  
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect  
 PT other PRO polypeptides, link bioactive molecules to cells expressing  
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.  
 PT lung, breast, prostate, cervical -  
 XX  
 PS Claim 3; Fig 437; 813bp; English.  
 XX  
 CC AAS21244-AAS21518 encode for novel human secretory and transmembrane  
 CC PRO polypeptides. The PRO polypeptides are useful to detect other  
 CC PRO polypeptides, to link bioactive molecules to cells expressing  
 CC PRO polypeptides, to modulate biological activities of cells expressing  
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,  
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
 CC polypeptide expression in a cell sample to that in a control sample.  
 CC Some of the 275 sequences are also useful to stimulate the release of  
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the  
 CC proliferation or differentiation of chondrocytes, the proliferation or  
 CC gene expression in pericyte cells, the release of proteoglycans from  
 CC cartilage, the proliferation of inner ear utricular supporting cells or  
 CC of T-lymphocytes, the release of a cytokine from peripheral blood  
 CC monocytes (PMCs), or the proliferation of endothelial cells. Some of  
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by  
 CC skeletal muscle cells or by adipocytes, or inhibit binding of A-peptide  
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify  
 CC molecules involved in binding interactions. The polynucleotides encoding  
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,  
 CC transgenic or knock out animals and can be used in gene therapy.  
 XX  
 SQ Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 6,73e-284 Length: 2185  
 Score: 3407.00 Matches: 648  
 Percent Similarity: 99.39% Conservative: 1  
 Best Local Similarity: 99.23% Mismatches: 4  
 Query Match: 98.87% Indels: 0  
 DB: 22 Gaps: 0  
 US-09-991-053-10 (1-653) x AAS21462 (1-2185)  
 QY 1 MetLysLeuLeuTTPGlnValThValHisHisThrTPsmaAlaIleLeuLeuPro 20  
 Db 57 ATGAAGCTCTTGTGAGTAACTGTGACACACACACTGAAATGACATCTGCTCCG 116  
 QY 21 PheValTyrLeuThrAlaGlnValTrrIleLeuGlyAlaAlaIleAlaAlaSer 40  
 Db 117 TTGCTTAACTTACGAGGCGCAAGTGTGATCTGTGTGAGCCATGCTGCGCTCA 176  
 QY 41 AlaGlyProGlnAanCyPProSerValCySerCySerAanGlnPheSerIleValVal 60  
 Db 177 GCCGGGCCCCGAACTGCCCTTGTGCTGCTGCACTAACCACTTACGAGAGGTGTG 236  
 QY 61 CysThrArgArgGlyLeuSerGluValProGlnGlyIleProSerAanThrArgTyrLeu 80  
 Db 237 TGCACGCGCCGGGGGCTCTCCGAGGTCCCGCAGGATATTCCTCGAACACCCGGTACTC 296

QY 81 AsnLeuMetGluAanAniIleGlnMetIleGlnAlaAspThrPheArgHisIleHis 100  
 Db 297 AACCTATGAGAAACAACATCCAGATATCATCGAGCGCAACCTTCGCCCATCTCACAC 356  
 QY 101 LeuGluValLeuGlnIleuGlyArgAanSerIleArgGlnIleGluValIleAlaPheAsn 120  
 Db 357 CTGAGAGTCTGACAGTGGGAGAGAACTCATCCGGAGATTGAGGTGGGGGCTTCAC 416  
 QY 121 GlyLeuAlaSerLeuSerThrLeuGluLeuPheAspAanThrPheValIleProSer 140  
 Db 417 GCGCTGACCGCTCAACACCTGAGACTTTGACACACTGCTGACAGTCACTTCCTAGC 476  
 QY 141 GlyAlaPheGluTyrLeuSerIleuArgGluLeuTrrPheuArgAanProIleGlu 160  
 Db 477 GGGGCTTTGAATACCTGTCACAGCTCGGAGCTGCTTGCTTGCAACACCCATCGAA 536  
 QY 161 SerIleProSerTyrAlaPheAanArgValProSerLeuMetArgLeuAspLeuGlyGlu 180  
 Db 537 AGCATCCCTCTTAACGCTTCAACCGGGTCCCTCTCATGCGCTTGAGCTTGGGGAG 596  
 QY 181 LeuIleValLeuGluTyrIleSerGluGlyAlaPheGluGlyLeuPheAanLeuTyr 200  
 Db 597 CTCAAGAGCTGAGATATATCTGAGGAGACTTTGAGGAGGCTGTTCACCTCAAGTAT 656  
 QY 201 LeuAanLeuGlyMetCysAanIleLysAspMetProAanLeuThrProLeuValGlyLeu 220  
 Db 657 CTGAACCTTGGGCACTGTCACCACTTAAGACATGCCAATCTCAACCCCTGTGGGCTG 716  
 QY 221 GluGluLeuGluMetSerGlyAanHisPheProGluIleArgProGlySerPheHisGly 240  
 Db 717 GAGAGAGTGAAGATGTGAGGAGAACCACTTCCCTGAGATCAAGGCTGCTCTTCATGCG 776  
 QY 241 LeuSerSerLeuValValSerTrrValMetAanSerIleValSerIleGluArgAsn 260  
 Db 777 CTGAGCTCCCTCAAGAGCTCTGGGTATGATAACTCAAGGTCAGCTGATGAGCGGAGAT 836  
 QY 261 AlaPheAspGlyLeuAlaSerIleValGluLeuAanLeuAlaHisAanLeuSerSer 280  
 Db 837 GCTTTTACGGGCTGGCTTCACTTGTGAGACTCACTTGGCCCAATTAACCTCTTCT 896  
 QY 281 LeuProHisAspLeuPheThrProLeuArgTyrLeuValGluLeuHisIleAsn 300  
 Db 897 TTGCCCCATGACCTTTTACCCCGCTGAGGATCACTGTGGAGTTGATCTACACACAAAC 956  
 QY 301 ProTrrAanCyAspPyrAspPyrIleLeuTrrPheuAlaTrrPrrPheuArgIlePro 320  
 Db 957 CTTTGAACCTGTGATTTGTGACATTTGTGCTTACCTGCTGAGCTTTCAGAGTATATACCC 1016  
 QY 321 ThrAanSerThrCysGlyArgCysHisAlaLapProMetHisMetArgGlyArgTyrLeu 340  
 Db 1017 ACCAATTCACCTGCTGTGCGCTGTGATGCTTCCATGACATGCAAGGCGGCTTACTC 1076  
 QY 341 ValGluValAspGlnAlaSerPheGlnCysSerAlaProPheIleMetAspAlaProArg 360  
 Db 1077 GTGAGAGTGAACCAAGCTCTCTTCCAGTGTCTGCCCCCTTCATCATGAGACACTGCA 1136  
 QY 361 AspLeuAanIleSerGluGlyArgMetAlaGluLeuLysCysArgTrrProPrrMetSer 380  
 Db 1137 GACCTCAACATTTCTGAGGGTGGATGAGCAAGATTGAAGTGTGCACTCCCTCATATGCC 1196  
 QY 381 SerValIysTrrPheLeuProAanGlyThrValLeuSerHisAlaSerArgHisProArg 400  
 Db 1197 TCCGTGAGTGTGCTGCTGCTGCAATGAGACAGTCTCAACCAAGCTCCGCGCAACAGG 1256  
 QY 401 IleSerValLeuAanAspGlyThrLeuAanPheSerHisValLeuLeuSerAspThrGly 420  
 Db 1257 ATCTCTGCTCAACGAGGACCTTGAACTTTCCACGAGTGTGCTTTCAGACACTGGG 1316  
 QY 421 ValTyrThrCysMetGlyThrAanValAlaGlyAanSerAanAlaSerAlaTyrLeuAsn 440  
 Db 1317 GTGTACACATGACAGTGAACCAATGTTGACAGCAACTCAACGCTCGGCTTACTCAT 1376  
 QY 441 GlySerThrAlaGluLeuAanThrSerAanTyrSerPhePheThrGlyThrGlyGlu 460



```

Db      1377 GTGAGCAGGCTGAGCTTAACACCTCCAACTACACTCTTCCACCAAGTAACAGTGGAG 1436
Qy      461 ThrThrgluIleSerProGluuAspThrThrgluValSerProValProThrThrSer 480
Db      1437 ACCGAGGAGATCTCGCTGAGGACACACGCGAAGTACAGCTCTTCTTACCAAGCTCC 1496
Qy      481 ThrGlyTyrGlnProAlaTyrThrThrSerThrValLeuIleGlnThrThrArgVal 500
Db      1497 ACTGGTACCAAGCCGGCATATACCACTTACCAAGTGCATTCATTCAGACTACCGGTGTG 1556
Qy      501 ProIysGlnValAlaValProAlaThrAspThrThrAspIysMetGlnThrSerLeuAsp 520
Db      1557 CCCAAGCAGGTGGCGAGTCCGCGACACACCACTGACCAAGATGACACAGCAGCTGGAT 1616
Qy      521 GluValMetIysThrThrIleIleIleIleGlyCysPheValAlaValThrLeuLeuAla 540
Db      1617 GAAAGTACGAAAGACCAACCAAGTCACTTGGCTCTTGGCGATCACTGCTGACT 1676
Qy      541 AlaAlaMetLeuIleValPheTyrIysLeuArgIysGlnGlnArgSerThrVal 560
Db      1677 GCCCGCATGTTGATGTCTTCTATTAACCTTGTAAAGCGGACACGAGGAGTACAGTC 1736
Qy      561 ThrAlaAlaArgThrValGluIleIleGlnValAspGluAspIleProAlaAlaThrSer 580
Db      1737 ACAGCGCCGCGAGCTGTGAGATATCCAGGTGACGAAACATCCCGACGACCAATCC 1796
Qy      581 AlaAlaIleThrAlaAlaProSerGlyValSerGlyGlnGlyAlaValValLeuProThr 600
Db      1797 GCAGCAGCAACAGCAGCTCCGTCGGATATCAGGTGAGGGGCGAGTGTGCTCCACA 1856
Qy      601 IleHisAspHisIleAsnTyrAsnThrTyrIysProAlaHisGlyAlaHisIleThrGlu 620
Db      1857 ATTGATGACCATATTATTACTACACACCTTAACAAACAGCACATGGGGCCCATCGGACAA 1916
Qy      621 AsnSerLeuGlyAsnSerLeuHisProThrValThrThrIleSerGluProTyrIleIle 640
Db      1917 AACGAGCTGGGAGACTCTCTGACCCCGACAGCACCACTATCTGAACTTATTAATT 1976
Qy      641 GlnThrHisThrIysAspIysValGlnGlnThrGlnIle 653
Db      1977 CAGACCCATACCAAGCAAGGTACGAGAACTCAATA 2015

RESULT 6
AAF44179 standard; cDNA; 2185 BP.
XX
AC AAF44179;
XX
XX 02-APR-2001 (first entry)
XX
DE Human PRO1111 (UNQ554) nucleotide sequence SEQ ID NO:228.
XX
XX Human, secreted and transmembrane protein; PRO; cytostatic;
XX KM cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
XX KM diagnostic assay; ss.
XX
XX Homo sapiens.
XX
XX WO200073454-A1.
XX
XX 07-DEC-2000.
XX
XX 30-MAR-2000; 2000WO-US08439.
XX
XX 02-JUN-1999; 99WO-US12252.
XX PR 23-JUN-1999; 99US-0141037.
XX PR 07-JUL-1999; 99US-0143048.
XX PR 20-JUL-1999; 99US-0144758.
XX PR 26-JUL-1999; 99US-0145698.
XX PR 28-JUL-1999; 99US-0146222.
XX PR 17-AUG-1999; 99US-0149396.
XX PR 15-SEP-1999; 99WO-US21090.

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PR 15-SEP-1999; 99WO-US21547.
PR 08-OCT-1999; 99US-0158663.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
XX
XX (GERTH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrata N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,
XX Germaidi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NP,
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
XX Zhang Z;
XX WPI; 2001-032160/04.
XX P-PSDB; AAB65217.
XX
XX PRO polynucleotides used to produce polypeptides used to target
XX PT bioactive molecules such as toxins, radiolabels or antibodies, to
XX PT specific cells, to cause targeted cell death -
XX
XX Claim 2; Fig 156; 935pp; English.
XX
XX The present invention describes human secreted and transmembrane PRO
XX CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
XX CC can be used for targeted delivery of bioactive molecules, such as
XX CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
XX CC sequences, and their fragments, can be used as hybridisation probes, in
XX CC chromosomal and gene mapping, and in the generation of anti-sense RNA
XX CC and DNA. They may also be used to produce transgenic animals which are
XX CC used to develop and screen therapeutically useful reagents. The PRO
XX CC nucleotide and protein sequence can be used for tissue typing and in
XX CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
XX CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
XX CC in the isolation of human PRO sequences. AAF44087 to AAF44469 and
XX CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
XX CC sequences given in the exemplification of the present invention.
XX
XX SQ Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;

Alignment Scores:
Pred. No.: 6,73e-284 Length: 2185
Score: 3407.00 Matches: 648
Percent Similarity: 99.39% Conservative: 1
Best Local Similarity: 99.23% Mismatches: 4
Query Match: 98.87% Indels: 0
DB: 22 Gaps: 0

US-09-991-053-10 (1-653) x AAF44179 (1-2185)
Qy 1 MethysLeuLeuTTPGlnValThrValHisHisIleThrTAspAlaIleLeuLeuPro 20
Db 57 ATGAAGCTCTTGGCGAGGTACGTGTACACCAACCACTCGAATGCCATCTCTCCCG 116
Qy 21 PheValTyrLeuThrAlaGlnValTrrPileuCyAlaAlaIleAlaIleAlaSer 40
Db 117 TTGCTTACCTCAAGCGGCAAGTGTGATTCGTGTGACAGCATCGCTGCGCGCTCA 176
Qy 41 AlaGlyProGlnAnCyProSerValCySerYserSerGlnGlnPheSerIysValVal 60
Db 177 GCCGGGCCCAAGACTCCCTCGTGTGCTCGTGTGAGTAACCAAGTTCAGCAAGGTGTG 236

```



QY 61 CyThrArgArgGlyLeuSerGluValProGlnGlyIleProSerAsnThrArgTyrLeu 80  
 Db 237 TGCACCGCGCGGGGCGCTCTCCGAGGTCCTCCGAGGATATCTCTCGAACACCGGTAACCTC 296  
 QY 81 AsnLeuMetGluAsnAsnIleGlnMetIleGlnAlaAspThrPheArgHisLeuHis 100  
 Db 297 AACCTATGAGAAACAATCCAGATGATCCAGCCGACACTTCCGCCCTCCACAC 356  
 QY 101 LeuGluValLeuGlnLeuGlyArgAsnSerIleArgGlnIleGluValAlaPheAsn 120  
 Db 357 CTGGAGGCTCTGAGATTGGCAGAGAACTCCATCCGAGATGAGGGGGGCTTCAC 416  
 QY 121 GlyLeuAlaSerLeuSerThrLeuGluLeuPheAspAsnTrpLeuThrValIleProSer 140  
 Db 417 GGCCTGGCCGACCTCAACACCTGGAGCTGTCGACAACTGGCTGACAGTCACTCCAGC 476  
 QY 141 GlyValaPheGluTyrLeuSerLysLeuArgGluLeuTyrLeuArgAsnAsnProIleGlu 160  
 Db 477 GGGGCGCTTTGAAATACCTGTCAGAGCTGGGAGCTGGCTGCGCAACACCCATCGAA 536  
 QY 161 SerIleProSerTyrAlaPheAsnArgValProSerLeuMetArgLeuAspLeuGlyLeu 180  
 Db 537 AGATACCCCTCTTAACGCTTCAACCGGGTCCCTCCCTCAATGCGCTTGAGGGGAG 596  
 QY 181 LeuLysLeuLeuGluTyrIleSerGluGlyAlaPheGluGlyLeuPheAsnLeuLysTyr 200  
 Db 597 CTCAAGAGCTGGAGATATCTCTGAGGAGGCTTTTGAAGGGCTGTTCAACCTCAAGTAT 656  
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 Db 717 GAGGAGCTGGAGATGTAGGAGAACCACTCCCTGAGATCAGGCTGCTCTTCCATGAC 776  
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 QY 261 AlaPheAspGlyLeuAlaSerLeuValGluLeuAsnLeuAlaHisAsnAsnLeuSerSer 280  
 Db 837 GCCTTTGACGGGCGCTTCACTGTGAACTCAACTGGCCCACTAATCACTCTCTTCT 896  
 QY 281 LeuProHisAspLeuPheThrProLeuArgTyrLeuValGluLeuHisLeuHisAsn 300  
 Db 897 TTGCCCATGACCTTTTACCCGCTGAGGATGCTGGTGAAGTTCATACACCAAC 956  
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 QY 361 AspLeuAsnIleSerGluArgMetAlaGluLeuLysCysArgTyrProProMetSer 380  
 Db 1137 GACCTCAACATTTCTGAGGCTCGATGCGAAGCTTAAGTGTGGAATCTCCCTCATATCTC 1196  
 QY 381 SerValIleTrpLeuLeuProAsnGlyThrValLeuSerHisAlaSerArgHisProArg 400  
 Db 1197 TCCGTGAAGTGTGCTGCCAATGGGACAGTCTCAAGCAAGCTCCGCCCAAGCAAG 1256  
 QY 401 IleSerValIleuAsnAspGlyThrLeuAsnPheSerHisValLeuLeuSerAspThrGly 420  
 Db 1257 ATCTCTGTCTCAACGAGGCACTTGAACCTTTCACAGTGTGCTTTCAAGACACTGGG 1316  
 QY 421 ValTyrThrCysMetGlyThrAsnValAlaGlyAsnSerAsnAlaSerAlaTyrLeuAsn 440

Db 1317 GTGTACACATGATGATGTGACCAATGTTGAGGCACTCCAAAGCCCTGAGCTCACTCAAT 1376  
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 Db 1377 GTGAGCAGCGCTGAGGTTTAACCTTCAACCTCAAGCTTCTTCAACCAAGTATACAGTGAG 1436  
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 QY 641 GlnThrHisThrLysAspLysValGlnGluThrGlnIle 653  
 Db 1977 CAGACCATACCAAGGACAAAGTACAGAACTCAATA 2015

RESULT 7  
 ID ACA03821 standard; cDNA, 2185 BP.  
 AC ACA03821;  
 XX  
 AC 23-MAY-2003 (first entry)  
 DT  
 XX  
 DE cDNA encoding human PRO polypeptide #219.  
 XX  
 KW Human; PRO polypeptide; secreted and transmembrane protein;  
 KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;  
 KW differentiation; chondrocyte; tumour; genetic disorder;  
 KW cytoskeletal; gene; ss.  
 OS Homo sapiens.  
 XX  
 PN US2003036180-A1.  
 XX  
 PD 20-FEB-2003.  
 XX  
 PF 09-MAY-2002; 2002US-0143114.  
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 PR 12-JUN-1998; 98MO-US12456.  
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PR 28-AUG-1998; 98WO-US17888.  
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 PR 24-FEB-2000; 2000WO-US05004.  
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 PR 15-MAR-2000; 2000WO-US06319.  
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 PR 30-MAY-2000; 2000WO-US14042.  
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 PR 28-JUL-2000; 2000WO-US15264.  
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 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 22-JUN-2001; 2001WO-US20116.

PR 29-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 PR 20-DEC-2000; 2000WO-US27259.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
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 PR 10-MAY-2001; 2001US-0854280.  
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 PR 19-DEC-2001; 2001US-0028072.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI: 2003-332040/31.  
 DR P-PSDB; ABU66788.  
 XX  
 PT New secreted and transmembrane PRO nucleic acids, useful for gene  
 PT therapy, in chromosome and gene mapping, as chromosome markers, in  
 PT tissue typing, and in chromosome identification  
 PT  
 XX  
 PS Claim 2; Fig 437; 660pp; English.  
 XX  
 CC The present invention relates to the isolation of novel human PRO  
 CC polypeptides, and the polynucleotide sequences encoding them. The  
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO  
 CC polypeptides are useful for detecting other PRO polypeptides, for  
 CC linking bioactive molecules to cells expressing PRO polypeptides,  
 CC for modulating biological activities of cells expressing PRO  
 CC polypeptides, and for identifying agonists or antagonists.  
 CC The PRO polypeptides are useful for stimulating the release of  
 CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating the  
 CC proliferation or differentiation of chondrocytes, and detecting the  
 CC presence of tumours. The polynucleotide sequences encoding PRO  
 CC polypeptides are useful as hybridisation probes, in chromosome and  
 CC gene mapping, in the generation of antisense RNA and DNA, in the  
 CC preparation of PRO polypeptides, for generating transgenic animals or  
 CC knockout animals, for the genetic analysis of individuals with genetic  
 CC disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs  
 CC encoding the human PRO polypeptides of the invention.  
 CC Note: The sequence data for this patent was obtained in electronic  
 CC format directly from the USPRO web site at  
 CC seqdata.uspto.gov/patident.html.  
 CC  
 XX  
 SQ Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;  
 XX  
 Alignment Scores:  
 Pred. No.: 6,73e-284 Length: 2185  
 Score: 3407.00 Matches: 648  
 Percent Similarity: 99.39% Conservative: 1  
 Best Local Similarity: 99.23% Mismatches: 4  
 Query Match: 98.87% Indels: 0  
 DB: 25 Gaps: 0  
 US-09-991-053-10 (1-653) x ACA03821 (1-2185)  
 Oy 1 MetLysLeuLeuTrpGlnValThrValIleIleHisIleThrTrpAsnAlaIleLeuLeuPro 20

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Db      57 ATAAACCTCTTGGAGGAGTAACCTGTCACACACACCTGGAATGCATCCCTGCTCCG 116
Qy      21 PheValTyrLeuThrAlaGlnValITripLeuCyAlaAlaAlaAlaAlaAlaSer 40
Db      117 TTCGTCTACCTCAGGGGCAAGTGTGATCTGTGTGCACCAATCGTGTGCGGCTCA 176
Qy      41 AlaGlyProGlnAsnCyProSerValCySerCySerAsnGlnPheSerLysVal 60
Db      177 GCCGGGCCCCAGAACTGCCCCCTCGTTTGTCTGGTGCAGTAACCAAGTTCAAGCAAGTGTG 236
Qy      61 CysThrArgArgGlyLeuSerGluValProGlnGlyLeuProSerLysThrArgTyrLeu 80
Db      237 TGCACCCGCGCGGGGCTCTCCGAGGTCGCCAGGGGTATTCCTCGAACACCCGGTACTTC 296
Qy      81 AsnLeuMetGluAsnAsnIleGlnMetIleGlnAlaAspThrPheArgHisIleHis 100
Db      297 AACCTCATGGAGAACACATCCAGATGATCCAGGCCACACCTTCGCCACCTCCACAC 356
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Db      357 CTGGAGGTCTCTGAGTTGGGCGAGAACTCATCCGAGATGAGTGGGGGCTTCAAC 416
Qy      121 GlyLeuAlaSerLeuSerThrLeuGluLeuPheAspAsnTrpLeuThrValIleProSer 140
Db      417 GGCCTGGCCAGCTCAACACCTGAGAGCTGTTCGACACATGGCTGACAGTCATCCCTAGC 476
Qy      141 GlyAlaPheGlnTyrLeuSerLysLeuArgGluLeuTrpLeuArgAsnAsnProIleGlu 160
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Qy      161 SerIleProSerTyrAlaPheAsnArgValProSerLeuMetArgLeuAspLeuGlyLeu 180
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Qy      341 ValGluValAspGlnAlaSerPheGlnCysSerAlaProHeiIleMetAspAlaProArg 360
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Db      1257 ATCTGTCTCTCAACAGACGCACTTGAACCTTTTCCAGTGTGCTTTCAGACATGGGG 1316
Qy      421 ValTyrThrCysMetGlyThrAsnValAlaGlyAsnSerAsnAlaSerAlaTyrLeuAsn 440
Db      1317 GTGTACACATGCAATGTGTGACCAATGTGCAAGGCAATCCCAACCGCTCGGCTACTCCAT 1376
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Db      1377 GTGAGCAGCGCTGAGCTTAACCTCACTCACTCAAGCTTCTTACCAACAGTAACGTGGAG 1436
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Qy      481 ThrGlyTyrGlnProAlaTyrThrThrSerThrValLeuIleGlnThrThrArgVal 500
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## RESULT 8

ACA04242  
ID ACA04242 standard; cdna, 2185 BP.

ACA04242;  
AC

27-MAY-2003 (first entry)  
DT

Human cdna encoding a secreted/transmembrane protein, SEQ ID 437.  
DE

Human; se; gene; secreted protein; transmembrane protein; PRO;  
inflammatory disease; organ failure; atherosclerosis; cardiac injury;  
infertility; birth defects; premature aging; AIDS; biosensor;  
acquired immunodeficiency syndrome; cancer; diabetic complication;  
bioreactor; tumour.  
KW

XX Homo sapiens.  
OS  
XX US2003032155-A1.  
PN  
XX 13-FEB-2003.  
XX  
PF 03-MAY-2002; 2002US-0137865.  
XX  
XX 31-MAR-1997; 97WO-US05230.  
PR 12-JUN-1998; 98WO-US12456.  
PR 14-JUL-1998; 98WO-US14552.  
PR 28-AUG-1998; 98WO-US17888.  
PR 10-SEP-1998; 98WO-US18824.  
PR 14-SEP-1998; 98WO-US19093.  
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PR 16-SEP-1998; 98WO-US19330.  
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PR 24-FEB-2000; 2000WO-US04914.  
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PR 15-MAR-2000; 2000WO-US06884.  
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PR 30-MAR-2000; 2000WO-US08439.  
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PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
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PR 28-FEB-2001; 2001WO-US06520.  
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PR 22-JUN-2001; 2001WO-US20116.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 20-DEC-2000; 2000US-0747259.  
PR 28-FEB-2001; 2001US-0796498.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 18-MAY-2001; 2001US-0860216.  
PR 25-MAY-2001; 2001US-0866028.  
PR 01-JUN-2001; 2001US-0872035.  
PR 05-JUN-2001; 2001US-0874503.  
PR 14-JUN-2001; 2001US-0882636.  
PR 19-JUN-2001; 2001US-0886342.  
PR 21-JUN-2001; 2001US-0887879.  
PR 18-JUL-2001; 2001US-0908827.  
PR 06-AUG-2001; 2001US-0924419.  
PR 09-AUG-2001; 2001US-0927796.  
PR 16-AUG-2001; 2001US-0931836.  
PR 19-DEC-2001; 2001US-0028072.  
XX  
XX (GENTH ) GENENTECH INC.  
PA  
XX Baker KP, Beresini M, DeForge L, Deanoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX  
XX WPI: 2003-331925/31.  
DR P-PSDB; ABU67064.  
XX  
XX New secreted and transmembrane nucleic acids and polypeptides,  
PT designated as PRO, useful for treating inflammation, organ failure,  
PT atherosclerosis, cardiac injury, infertility, birth defects, premature  
PT aging, AIDS, or cancer  
XX  
PS Claim 2; Fig 437; 659pp; English.  
XX  
XX The invention relates to an isolated nucleic acid comprising, or which is  
CC at least 80% identical to, or the full-length coding sequence of, any of  
CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide  
CC (one of 275 secreted or transmembrane proteins). The nucleic acid  
CC further comprises the full-length coding sequence of the DNA deposited  
CC under American Type Culture Collection (ATCC) accession number in a list  
CC given in the specification. Also included are vectors and host  
CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO  
CC antibodies, PRO extracellular domains and mature sequences, methods  
CC of detecting PRO proteins, methods for stimulating the release of  
CC TNF-alpha (tumour necrosis factor alpha) from human blood,  
CC (and the proliferation of differentiation of chondrocyte cells, the  
CC proliferation of, or gene expression in pericyte cells, the release or  
CC proteoglycans from cartilage, proliferation of inner ear utricular  
CC supporting cells, the proliferation of T-lymphocyte cells, the release  
CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the  
CC proliferation of endothelial cells), a method for modulating the uptake  
CC of glucose or free fatty acid (FFA) by skeletal muscle cells,  
CC a method for inhibiting the binding of A-peptide to factor VIIa,  
CC or the differentiation of adipocyte cells, a method for detecting the  
CC presence of a tumour in a mammal and an oligonucleotide probe derived

CC from any of the nucleotide sequences cited above. The nucleic acids and  
 CC polypeptides are useful for treating inflammatory diseases, organ  
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,  
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or  
 CC diabetic complications. The nucleic acids are useful as hybridisation  
 CC probes, in chromosome and gene mapping, and in generating antisense RNA  
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,  
 CC biosensors or bioreactors. Both are useful in tissue typing.  
 CC The present sequence encodes a PRO protein of the invention.

XX Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;

# Alignment Scores:

Pred. No.:	6,73e-284	Length:	2185
Score:	3407.00	Matches:	648
Percent Similarity:	99.39%	Conservative:	1
Best Local Similarity:	99.23%	Mismatches:	4
Query Match:	98.87%	Indels:	0
DB:	25	Gaps:	0

US-09-991-053-10 (1-653) x ACA04242 (1-2185)

QY 1 MellyleuLeuLeuTPGlnValThrValHISHisThrTrpAsnAlaIleLeuLeuPro 20  
 DB 57 ATGAAGCTCTTGCGAGTAACTGTGCACACCACTGGAATGCCATCTGCTCCG 116  
 QY 21 PheValTyrLeuThrAlaGlnValTrpIleLeuCyAlaIleAlaIleAlaSer 40  
 DB 117 TTGCTTAACTCAGCGGCGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 176  
 QY 41 AlAGlyProGlnAsnCyProSerValCySerCySerAsnGlnPheSerValVal 60  
 DB 177 GCGGGGCGCCAGAACTGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 236  
 QY 61 CyThrArgArgGlyLeuSerGluValProGlnGlyIleProSerAsnThrArgTyrLeu 80  
 DB 237 TGCACGGCGCGGGGCTCTCCAGAGTCCCGAGGATTCCTCGAACCACCGGTACTC 296  
 QY 81 AsnLeuMetGlnAsnAsnIleGlnMetIleGlnAlaSerThrPheArgHisIleuHis 100  
 DB 297 AACCTCATGAGAACAAATCATCATGATCATGAGCGACACTTCCGCACTTCACAC 356  
 QY 101 LeuGluValLeuGlnLeuGlyArgAsnSerIleArgGlnIleGluValAlaPheAsn 120  
 DB 357 CTGAGAGTCCCTGACGTTGGGAGGAACTCCATCCGGAGATGAGTGGGGGCTTAC 416  
 QY 121 GlyLeuAlaSerLeuSerThrLeuGluLeuPheAsnTrpLeuThrValIleProSer 140  
 DB 417 GGCCTGGCCAGCTCAACACCTGTGAGCTGTTCGACAACTGGCTGACAGTATCCTAGC 476  
 QY 141 GAlaAlaPheGlnTyrLeuSerIleValArgGluLeuTrpLeuArgAsnProIleGlu 160  
 DB 477 GGGGCTTTGAATACCTGCAAGCTCGGAGCTGTGGCTGCAACACCCCATGAA 536  
 QY 161 SerIleProSerTyrAlaPheAsnArgValProSerLeuMetArgLeuAspLeuGlyIle 180  
 DB 537 AGCATCCCTCTTAACGCTTCAACCGGCTGCTCCCTCATGCGCTGAGCTTGGGGAG 596  
 QY 181 LeuIleValLeuGlnTyrIleSerGlnGlyAlaPheGlnGlyLeuPheAsnLeuTyr 200  
 DB 597 CTCAGAGAGCTGGAGTATCTCTGAGAGGAGCTTTTGAAGGGGCTGTTCAACCTCAATAT 656  
 QY 201 LeuAsnLeuGlyMetCysAsnIleValAspMetProAsnLeuThrProLeuValGlyLeu 220  
 DB 657 CTGAATCTGGGAGTGCATTAAGACATGACCAATTCACCCCTGGTGGGCTG 716  
 QY 221 GlnGluLeuGlnMetSerGlyAsnHisPheProGluIleArgProGlyIleSerPheHisGly 240  
 DB 717 GAGAGAGTGAAGAGTCAAGGAACTCCCTCATGATCAGAGCTGCTGCTTCCATGCG 776  
 QY 241 LeuSerSerLeuIleValLeuTrpValMetAsnSerGlnValSerLeuIleGlnArgAsn 260  
 DB 777 CTGAGTCCCTCAAGAGAGCTCTGGGTATGAACTCAGAGTCAAGCTGATGAGCGGAAT 836

QY 261 AlaPheAspGlyLeuAlaSerLeuValGluLeuAsnLeuAlaHisAsnLeuLeuSer 280  
 DB 837 GCTTTGAGCGGGCTGCTTCACTTGTGAACTCACTTGGCCCAATAAACCCTCTTCT 896  
 QY 281 LeuProHisAspLeuPheThrProLeuArgTyrLeuValGluLeuHisIleuHisAsn 300  
 DB 897 TTGCCCCATGACCTCTTACCCCGCTGAGGATCCTGTGTGAGTGTGATCAACCAAC 956  
 QY 301 ProTrpAsnCyAspAspIleLeuTrpLeuAlaTrpTrpLeuArgGlnTyrIlePro 320  
 DB 957 CTTGGAAGCTGATGTGATGATCTGTGCTAGAGCTGTGGTGTGAGATATATACC 1016  
 QY 321 ThrAsnSerThrCysCySerGlyArgCysHisAlaProMetHisMetArgGlyArgTyrLeu 340  
 DB 1017 ACCAATTTCAACCTGCTGTGGCGCTGCTCATGCTCCATGCACATGGAGGCGCTTACTC 1076  
 QY 341 ValGluValAspGlnAlaSerPheGlnCysSerAlaProPheIleMetAspAlaProArg 360  
 DB 1077 GTGAGGTGAGCCAGGCTCTCTCCAGTGTCTGCCCCCTTCATATGAGCGACCTCGA 1136  
 QY 361 AspLeuAsnIleSerGlnGlyArgMetAlaGluLeuLeuCyArgThrProProMetSer 380  
 DB 1137 GACCTCAACATTTCTGAGGGTGGATGGAGCAACTTAAGTGTGCACTCCCTATGTCC 1196  
 QY 381 SerValIleTrpLeuLeuProAsnGlyThrValLeuSerHisAlaSerArgHisProArg 400  
 DB 1197 TCCGTGAAGTGTGTCTGCCCAATGGAGACAGTCTTACGCCACGCTTCCGCCACCAAG 1256  
 QY 401 IleSerValLeuAsnAspGlyThrLeuAsnPheSerHisValLeuLeuSerAspThrGly 420  
 DB 1257 ATCTGTCTCTCAACGACGCGCACTTGAACCTTTTCCAGTGTCTTCCAGACACTGGG 1316  
 QY 421 ValTyrThrCysMetGlyThrAsnValAlaGlyAsnSerAsnAlaSerAlaTyrLeuAsn 440  
 DB 1317 GTGTACACATGATGTGACCAATGTGTGACAGGCAACTCCAAACCTCGGCTTACTCAAT 1376  
 QY 441 GlySerThrAlaGluLeuAsnThrSerAsnTyrSerPhePheThrGlyThrGlyGlu 460  
 DB 1377 GTAGACAGGCTAGCTTAACCTTCACTCACTCACTTCTTACCAACAGTAACAGTGGAG 1436  
 QY 461 ThrThrGlnIleSerProGlnAspThrThrArgIleTyrIleAspProValProThrThrSer 480  
 DB 1437 ACCACGAGATCTCGCTGAGACACACGCGAAGTAAGTCAAGCTGTCTTACACAGTCC 1496  
 QY 481 ThrGlyTyrGlnProAlaTyrThrThrSerThrThrValLeuIleGlnThrThrArgVal 500  
 DB 1497 ACTGTTTACCGAGCGGATATATACCTTACACGAGTGTCTCATTCAGACTACCCGCTG 1556  
 QY 501 ProIleGlnValAlaValProAlaThrAspThrThrAspIleMetGlnThrSerLeuAsp 520  
 DB 1557 CCCAAGAGGTGGACAGTACCCGCGACACACCACTGACAAAGTACAGACACCTGGAT 1616  
 QY 521 GluValMetIleThrThrIleIleIleGlyCysPheValAlaValThrLeuLeuAla 540  
 DB 1617 GAGTATGAGAACACCAAGATCATCTTGGCTGCTTGTGGCAGTGTCTGTAGCT 1676  
 QY 541 AlaIleMetIleValPheTyrIleValArgIleValArgHisGlnGlnArgSerThrVal 560  
 DB 1677 GCCGCAATGTGATTTCTTCTTAACCTTGTAAACCTGTAACCGGACACGAGCGAGTACAGTC 1736  
 QY 561 ThrAlaAlaArgThrValGluIleIleGlnValAspGluAspIleProAlaAlaThrSer 580  
 DB 1737 ACAAGCGCCGAGCTGTGATTAATCCAGTGAAGAAACATCCAGAGGAAACATTC 1796  
 QY 581 AlaAlaAlaThrAlaAlaProSerGlyValSerGlyGluGlyValAlaValLeuProThr 600  
 DB 1797 GAGAGAGAACACAGACTCCGCTGCTATCAAGTGAAGGGGCAAGTGTGTGTGCCACA 1856  
 QY 601 IleHisAspHisIleAsnTyrAsnThrTyrIleProAlaHisGlyAlaHisIleTrpThrGlu 620  
 DB 1857 ATTCAATGACATATTAATCAACACCTTAACCAACGACATGGGGGCCCACTGAGACGAA 1916

QY 621 Aasnserleugiyaasnserleuhsifrothryvalthrhrilesgergiupforyille 640  
Db 1917 AACAGCTGGGAACTCTCTGACCCACAGTACCACTTATCTGAACTTATATAT 1976  
QY 641 GlnThrHsthrlysaaplyvalGlnGlnThrGlnlle 653  
Db 1977 CAGACCCATACCAAGACAGGATACGAACTCAATA 2015

RESULT 9  
ABX89359  
ID ABX89359 standard; cDNA, 2185 BP.  
XX  
AC ABX89359;  
XX  
DT 13-MAY-2003 (first entry)  
XX  
DE DNA encoding novel secreted and transmembrane protein PRO111.  
XX  
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ss.  
XX  
OS Homo sapiens.  
XX  
FN US2003017563-A1.  
XX  
PD 23-JAN-2003.  
XX  
PF 07-MAY-2002; 2002US-0140808.  
XX  
XX 31-MAR-1997; 97WO-US05230.  
PR 12-JUN-1998; 98WO-US12456.  
PR 14-JUL-1998; 98WO-US14552.  
PR 28-AUG-1998; 98WO-US17888.  
PR 10-SEP-1998; 98WO-US18824.  
PR 14-SEP-1998; 98WO-US19093.  
PR 14-SEP-1998; 98WO-US19094.  
PR 14-SEP-1998; 98WO-US19177.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 29-OCT-1998; 98WO-US22991.  
PR 29-OCT-1998; 98WO-US22992.  
PR 20-NOV-1998; 98WO-US24855.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 10-MAR-1999; 99WO-US05190.  
PR 20-APR-1999; 99WO-US08615.  
PR 14-MAY-1999; 99WO-US10733.  
PR 02-JUN-1999; 99WO-US12252.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 13-SEP-1999; 99WO-US20944.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28409.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 02-DEC-1999; 99WO-US28551.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.  
PR 20-DEC-1999; 99WO-US30999.  
PR 22-DEC-1999; 99WO-US30720.  
PR 30-DEC-1999; 99WO-US31243.  
PR 30-DEC-1999; 99WO-US31274.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 01-MAR-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05746.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US15264.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUN-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23532.  
PR 24-AUG-2000; 2000WO-US23338.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06666.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 22-JUN-2001; 2001WO-US20116.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 20-DEC-2000; 2000WO-US074259.  
PR 28-FEB-2001; 2001US-0796498.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854280.  
PR 18-MAY-2001; 2001US-0860216.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 01-JUN-2001; 2001US-0872035.  
PR 05-JUN-2001; 2001US-0874503.  
PR 14-JUN-2001; 2001US-0882636.  
PR 19-JUN-2001; 2001US-0886342.  
PR 21-JUN-2001; 2001US-0887879.  
PR 18-JUL-2001; 2001US-0908827.  
PR 06-AUG-2001; 2001US-0924419.  
PR 09-AUG-2001; 2001US-0927796.  
PR 16-AUG-2001; 2001US-0931836.  
PR 19-DEC-2001; 2001US-0028072.

XX (GERTH ) GENENTECH INC.  
XX  
XX Baker KP, Beresini M, DeForge L, Deenoyers L, Filvaroff B, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX WPI; 2003-148238/14.  
XX P-PSDB; ABUS9869.

PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1366 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
PT are therapeutically useful for enhancing immune response and in cancer treatments

PS Claim 2; Fig 437; 659pp; English.

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO112 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186 stimulate adrenal cortical capillary endothelial growth, and PRO536, PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO825, PRO819, PRO1126, PRO1360 and PRO1387 induce C-fos in endothelial cells, and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating cancerous tumours. PRO812 inhibits vascular endothelial growth factor (VEGF) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth in mammals which would be beneficial in inhibiting tumour growth. PRO826, PRO1068, PRO1184, PRO1346 and PRO1355 stimulate proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of retinal neurons cells (PRO1132 is also enhances survival/proliferation of rod photoreceptor cells) and therefore are useful for treating retinal disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813 and PRO1106 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathias associated with dermatitis, herpetiformis or Crohn's disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This sequence encodes a novel human PRO protein.

**SQ** Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;

### Alignment Scores:

Pred. No.:	6.73e-284	Length:	2185
Score:	3407.00	Matches:	648
Percent Similarity:	99.35%	Conservative:	1
Best Local Similarity:	99.23%	Mismatches:	4
Query Match:	98.87%	Indels:	0
DB:	25	Gaps:	0

US-09-991-053-10 (1-653) X ABX89359 (1-2185)

QY	1	MeLysLeuLeuTrpGlnValThrValIshShiSrtTrtPAspAlaIleLeuLeuPro	20
Db	57	ATGAACTCTTGGGAGGTAACGTGGACCAACACACTGGAAATGCATCTCTCCG	116
QY	21	PheValTyrLeuThrLacIlnValTrpIleLeuCyValAlaIleAlaIleAlaSer	40
Db	117	TTGTGTACTCTACGGCGGCAAGTGGGAATTCGTGTGACGCAATCGCTGCGCGCTCA	176
QY	41	AlaGlyProGlnAsnGlySerProSerValCysSerCysSerAsnGlnPheSerLeuVal	60
Db	177	GCGGGGCCCAAGAACTGCCCTTCCTCGTTCTCTGTGCAATACGATTCAGCAAGTGGTG	236
QY	61	CysThrArgArgGlyLeuSerGluValProGlnGlyIleProSerAsnThrArgTyrLeu	80
Db	237	TGCACGCGCGGGGCTCTCCAGAGCTCCGCAAGGATATTCCTCCAAACCCGGTACTTC	296
QY	81	AsnLeuMetGluAsnAsnIleGlnMetIleGlnIleAspThrPheArgHsLeuHsShiS	100
Db	297	AACTCATGGAAGAACAATCCAGATGATCCAGCGCCACACTTCCGCCACTTCACAC	356
QY	101	LeuGluValLeuGlnLeuGlyArgAsnSerIleArgGlnIleGluValGlyAlaPheAsn	120
Db	357	CTGAAGTCTCTGAAGTTGGCAGGAATCATTCCGCAAGATTGAAGTGGGGGCTCTCAAC	416

QY	12	GIYleuNlaSerLeuSerThrLeuGluLeuPheAspAsnTrpLeuThrValIleProSer	140
Db	417	GGCCCTGGACACCTTCAACACCCTGGAGCTGTGGACAACCTGGCTGACAGTCATCC	476
QY	141	GIYAlaPheGluTrpLeuSerTrpLeuArgGluLeuTrpLeuArgAsnAsnProIleGlu	160
Db	477	GGGGCCTTTGAATACCTGTCCAGAGCTCCGGGAGCTTGGCTTGGCAACAACCCATGGAA	536
QY	161	SerIleProSerTrpAlaPheAsnArgValProSerLeuMetArgLeuAspLeuGlu	180
Db	537	AGCATCCCTCTTACGCTTCAACCGGAGTGGCCCTCCCTCATGCGCCTGAACTTGGGGAG	596
QY	181	LeuYerTrpLeuGluTrpTrpIleSerGluGluAlaPheGluGluLeuPheAsnLeuTrp	200
Db	597	CTCAAGAGAGCTGGAGTATCTCTGAGGGAGCTTTTAAAGGGCTGTTCACCTCAAGTAT	656
QY	201	LeuAsnLeuGluMetCysAsnIleLysAspMetProAsnLeuThrProLeuValIleu	220
Db	657	CTGAACCTTGGGCATGTGCACATTAAAGACATGCCCAATCTCACCCCCCTGTGGGGCTG	716
QY	221	GluGluLeuGluMetSerGlyAsnHisPheProGluIleArgProGlySerPheHisGly	240
Db	717	GAGAGAGCTGAGATGTCAAGGAAACCACTCCCTGATGATCAGAGCTGGCTCTTCATGGC	776
QY	241	LeuSerSerLeuYerIblybLeuTrpValMetAsnSerGluTrpValSerLeuIleGluArgAsn	260
Db	777	CTGAGCTCCCTCAAGAAAGCTCTGGGTATGAACTCAAGGTCACAGCTGATTTGACGGGAAT	836
QY	261	AlaPheAspGlyLeuAlaSerLeuValGluLeuAsnLeuAlaHisAsnAsnLeuSerSer	280
Db	837	GCTTTTACGGGGCTGGCTTCACTTGTGAACTCACTTGGCCCAATTAACCTCTCTCT	896
QY	281	LeuProHisAspLeuPheThrProLeuArgTrpLeuValGluLeuHisAsn	300
Db	897	TTGCCCATGACCTCTTACCCCGCTGAGTACCTGGAGGATTCATCTACACACAC	956
QY	301	ProTrpAsnCysAspCysAspIleLeuTrpLeuAlaTrpTrpLeuArgGluTrpIlePro	320
Db	957	CCTTGAACCTGTGATTGTGACATTCCTGTGGCTACCCGTGAGGCTTCAAGATATATACC	1016
QY	321	ThrAsnSerThrCysGlyArgCysHisAlaIleProMetHisMetArgGlyArgTrpLeu	340
Db	1017	ACCAATTCACCTCTGTGGCCGCTGTCAAGCTCCATGCACATGACAGAGGGCGCTACCTC	1076
QY	341	ValGluValAspGluAlaSerPheGluCysSerAlaProPheIleMetAspAlaProArg	360
Db	1077	GTGGAGGTGGACCAAGGCTCTTCCAGTGCCTGCCCTTCAATCAATGAGAGCACCTGCA	1136
QY	361	AspLeuAsnIleSerGluGlyArgMetAlaGluLeuLysCysArgTrpProProMetSer	380
Db	1137	GACCTCAACATTTCTGAGGGTCGGATGGCAGAACTTAAAGTGTGCGACTCCCCATATGCC	1196
QY	381	SerValIlystrPheLeuLeuProAsnGlyThrValLeuSerHisAlaSerArgHisProArg	400
Db	1197	TCCGGGAAGTGTGTGCCCCAATGGACATGTGTCAAGCAAGCTCCCGCCACCCAAAG	1256
QY	401	IleSerValLeuAsnAspGlyThrLeuAsnPheSerHisValLeuLeuSerAspThrGly	420
Db	1257	ATCTCTGTCCCAACAGAGCGACCTTGAACCTTTCCACAGTGTGCTTTCAAGACACTGGG	1316
QY	421	ValTrpThrCysMetGlyThrAsnValAlaGluAsnSerAsnAlaSerAlaTrpLeuAsn	440
Db	1317	GTGTAACATCATGATGACCAATGTTGGACAGGCAACTCAACGCGCTGGCTTCACTCAAT	1376
QY	441	GlySerThrAlaGluLeuAsnThrSerAsnTrpSerPhePheThrTrpGlyThrGlyGlu	460
Db	1377	GTGAGCACGGCTGAGCTTAACACTCCACATCAAGCTTCTTCAACCAAGTAACAGTGGAG	1436
QY	461	ThrThrGluIleSerProGluAspThrThrArgTrpYerTrpLysProValProThrThrSer	480
Db	1437	ACCAAGGAGATCTGCGCTGAGGACACAACGGGAAGTACAAGCTGTCTCTCAACAGCTCC	1496
QY	481	ThrGlyTrpGluProAlaTrpThrThrSerThrValLeuIleGluInThrThrArgVal	500

Db 1497 ACTGGTTCACGACCGCATATACCACTCTACCAAGGAGTCTCATTCACAGACTACCCGTGTG 1556  
Qy 501 ProlysglnValAlaValProAlaThrAspThrThrAspLysMetGlnThrSerLeuAsp 520  
Db 1557 CCCAGCGAGTGGCGACTCCCGCCAGACACCACTGTCACAGATCACAAGCAGCCTGGAT 1616  
Qy 521 GluValMetLysThrThrLysIleIleIleGlyCysPheValAlaValThrLeuVala 540  
Db 1617 GAAGTCATGAAGACCAACCAAGTATCATTTGGCTCTTTGGGAGGTACTGTGTAAGT 1676  
Qy 541 AlaAlaMetLeuIleValPheTyrIleLeuArgLysArgIleGlnGlnArgSerThrVal 560  
Db 1677 GCCCGCAAGTGTATGTTCTTCTTAACCTGTAAAGCGGACCAACGCGAGCAATCC 1736  
Qy 561 ThrAlaAlaArgThrValGluIleIleGlnValAspGluAspIleProAlaAlaThrSer 580  
Db 1737 ACAGCGCCCGGACCTGTGAATATCCAGGTGACGAGACGAGACATCCAGCAATCC 1796  
Qy 581 AlaAlaAlaThrAlaAlaProSerGlyValSerGlyGluAlaValAlaLeuProThr 600  
Db 1797 GCAGCAGCAACAGCAGCTCCGTCGGTATCAGGTGAGGGGGCAGTACTGCCACA 1856  
Qy 601 IleHisAspHisIleAsnTyrAsnThrTyrIlyAspProAlaHisIleGlyAlaHisTyrThrGlu 620  
Db 1857 ATTCATGACCATATTACTACCAACACCTCAACAAACGACGACATGGGCCCACTGGACAGAA 1916  
Qy 621 AsnSerLeuGlyAsnSerLeuHisProThrValThrThrIleSerGluProTyrIleIle 640  
Db 1917 AACAGCTGGGGAATCTCTTGACCCCAACAGTACACCATATCTGAACTTATTAAT 1976  
Qy 641 GlnThrHisThrLysAspLysValGlnGluThrGlnIle 653  
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RESULT 10  
ABX80270  
ID ABX80270 standard; DNA; 2185 BP.  
XX AC ABX80270;  
XX DT 28-APR-2003 (first entry)  
XX DE Novel human secreted or transmembrane protein PRO1344 DNA.  
XX KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-Fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Cronin's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.  
XX OS Homo sapiens.  
XX PN US2002132252-A1.  
XX PD 19-SEP-2002.  
XX PF 14-NOV-2001; 2001US-0990442.  
XX PR 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
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PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
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PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
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PR 28-APR-1998; 98US-083322P.  
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PR 28-MAY-1998; 98US-087106P.  
PR 02-JUN-1998; 98US-087607P.  
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PR 03-JUN-1998; 98US-087827P.  
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PR 04-JUN-1998; 98US-088033P.  
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PR 11-JUN-1998; 98US-088861P.  
PR 11-JUN-1998; 98US-088876P.  
PR 12-JUN-1998; 98US-089105P.  
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PR 16-JUN-1998; 98US-089512P.



PR 16-JUN-1998; 98US-089514P.  
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 PR 17-JUN-1998; 98US-089600P.  
 PR 17-JUN-1998; 98US-089653P.  
 PR 18-JUN-1998; 98US-089801P.  
 PR 18-JUN-1998; 98US-089907P.  
 PR 18-JUN-1998; 98US-089908P.  
 PR 28-AUG-2001; 2001US-0941992.  
 (GERTH ) GENENTECH INC.  
 PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Fong S, Garber H, Gerltsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurley AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 PI Zhang Z;  
 XX WPI: 2003-247083/24.  
 DR P-PSDB; ABUS9111.  
 XX  
 PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
 PT are therapeutically useful for enhancing immune response and in cancer  
 PT treatments  
 XX  
 PS Claim 2; Fig 158; 648pp; English.  
 XX  
 CC The invention describes an isolated human PRO polypeptide. The PRO  
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in  
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
 CC in modulating at least one biological activity of a cell expressing a PRO  
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
 CC stimulate adrenal cortical capillary endothelial growth, and PRO536,  
 CC PRO943, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
 CC useful for treating conditions or disorders where angiogenesis would be  
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
 CC useful for treating cancerous tumours. PRO812 inhibits vascular  
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
 CC cells and is thus useful for inhibiting endothelial cell growth in  
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing  
 CC immune response. PRO826, PRO1068 or PRO1132 enhance survival of  
 CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
 CC rod photoreceptor cells) and therefore are useful for treating retinal  
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
 CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,  
 CC and therefore are useful for treating kidney disorders associated with  
 CC decreased mesangial cell function such as Berger disease or other  
 CC nephropathies associated with dermatitis, herpetic forms or Crohn's  
 CC disease. PRO1034, PRO1312, PRO1192 and PRO1387 induce the  
 CC proliferation and/or redifferentiation of chondrocytes in culture and  
 CC are thus useful for treating sports injuries, and arthritis. This  
 CC sequence represents a novel human PRO protein polynucleotide.  
 XX  
 SQ Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;

## Alignment Scores:

Pred. No.: 6.73e-284 Length: 2185  
 Score: 3407.00 Matches: 648  
 Percent Similarity: 99.39% Conservative: 1  
 Best Local Similarity: 98.23% Mismatches: 4  
 Query Match: 98.87% Indels: 0  
 DB: 25 Gaps: 0

US-09-991-053-10 (1-653) x ABX80270 (1-2185)

Qy 1 MetIysleuLeuTrpGlnValThrValHisHisIstHrTrpAsnAlaIleLeuLeuPro 20

Db 57 ATGAGAGCTCTTGGCAGGTAACTGTGACACACACCTGGAATGCATCTGCTCCG 116  
 Qy 21 PheValTyrlleuThrAlaGlnValTrpIleLeuCyAlaAlaIleAlaAlaSer 40  
 Db 117 TTGGTCACTCACTGAGGCAAGTGTGATTCGTGTGACCACTGCTGTGCGCTCA 176  
 Qy 41 AlagIyProGlnAnCySProSerValCySerCySerAnGlnPheSerIyVal 60  
 Db 177 GCGGCGCCCAAGAACTGCCCTCCGTTGCTGCTGAGTAAACAGTTTACAGAGTGTG 236  
 Qy 61 CyeThrArgArgIyLeuSerGlnValProGlnGlyIleProSerAnThrArgTyLeu 80  
 Db 237 TGCAAGCGCGGGAGCTCTCCGAGGTCCGACAGGTATTCCTTCGAACACCGGTATCCTC 296  
 Qy 81 AsnLeuMetIuSerAnIleGlnMetIleGlnAlaAspThrPheArgHis 100  
 Db 297 AACCTCATGAGAACCAATCCAGATGATCCAGCCGACACTTCCGCCACTCCACAC 356  
 Qy 101 LeuGluValLeuGlnLeuGlyArgAnSerIleArgGlnIleGluValAlaPheAsn 120  
 Db 357 CTGGAGGTCTTGCAGTTGGGCAAGAACTCCATCCGCAAGTTAGGTGGGGCTTCAAC 416  
 Qy 121 GlyLeuAlaSerLeuSerThrLeuGlnLeuPheAspAnTrpLeuThrValIleProSer 140  
 Db 417 GGCTGGCCAGCTCAACACCTGAGCTGTTCGACAACTGGCTGACAGTCATCCTAGC 476  
 Qy 141 GlyAlaPheGluTyrlleuSerIySleuArgIleuTrpLeuArgAnAnProIleGlu 160  
 Db 477 GGGGCTTTAAATCACTGCAAGCTGGGAGCTCGCTTGGCAACACCCCATGAA 536  
 Qy 161 SerIleProSerTyrlaPheAnArgValProSerIleuMetArgLeuAspLeuGlu 180  
 Db 537 AGCATCCCTTACGCTTCAACCGGCTCCCTCTCATGGCCCTGAGCTTGGGGAG 596  
 Qy 181 LeuIySleuGluTyrlleuSerGluIyAlaPheGluIyLeuPheAnLeuTy 200  
 Db 597 CTCAAGAACTGGAGTATCTCTGAGGAGCTTTTGAAGGGCTTCAACCTCAAGTAT 656  
 Qy 201 LeuAnLeuGlyMetCySAnIleIySAspMetProAnLeuThrProLeuValGlyLeu 220  
 Db 657 CTGAACCTTGGGATGTGCAACATTAAAGACATGCCAATCTCAACCCCTGCTGGGCTG 716  
 Qy 221 GlnGluLeuGlnuetsArgIyAnHisPheProGlnIleArgProGlySerPheHisGly 240  
 Db 717 GAGAGCTGAGAGTATGAGGAACCTTCCGAGTACAGGCTGCTCTTCAAGGC 776  
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 Db 777 CTGAGCTCCCTCAAGAACTCTGGGTATGATCACTCAAGCTCAGCTGATTGAGCGAAT 836  
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 Qy 341 ValGluValAspGlnAlaSerPheGlnCySerAlaProPheIleMetAspAlaProArg 360  
 Db 1077 GTGAGGTGACAGGCTCTTCCAGTGTCTGCCCCCTTCAATCAAGACGACCTCGA 1136  
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 Qy 381 SerVallylSTrpleuLeuProAsnGlyThrValleuSerHisAlaSerArgHisProArg 400  
 Db 1197 TCCGGGAAGTGCTGCTCCCAATGGGACAGTGTCTCACCCACGCTCCCGCCACCCCAAGG 1256  
 Qy 401 IleserValleuAsnAspGlyThrleuAsnPheserHisValleuLeuSerAspThrGly 420  
 Db 1257 ATCTGTCTCAACAGCAGCGGACCTTGAACTTTTCCACGTGCTGCTTTGACAGACTGGG 1316  
 Qy 421 ValTYrThrCysMetGlyThrAsnValAlaGlyAsnSerAsnAlaSerAlaTYrleuAsn 440  
 Db 1317 GTGTACACATGATGATGTACCAATGTTCAGGCACTCCACGCTCGGCTTACTCTCAT 1376  
 Qy 441 GlySerThrAlaGlyLeuAsnThrSerAsnTYrSerPhePheThrThrGlyTYrGly 460  
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 Db 1737 ACAGCCGCCGCGACTTGAATATCCAGGTGGACGAGACATCCGACGACCAATCTCC 1796  
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 Db 1857 ATTCAATGACCAATTAATTAACCAACCTTAACCAACAGACATGGGGCCACTGGACAGAA 1916  
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 Db 1917 AACAGCCTGGGAACTCTCTGCAACCCCAAGTACCACTATCTGAACTTATTAATTT 1976  
 Qy 641 GlnThrHisThrLysAspLysValGlnGlnThrGlnIle 653  
 Db 1977 CAGACCCATACCAAGACAGAAAGTACAGGAACTCAATAA 2015  
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 ABX80774 ID ABX80774 standard; CDNA; 2185 BP.  
 XX AC ABX80774;  
 XX 22-APR-2003 (first entry)  
 DE Human secreted/transmembrane protein CDNA, #93.  
 XX Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;  
 KW diagnostic; biosensor; bioreactor; tumour; therapeutic;  
 KW gene therapy; tumour-associated antigenic target; TAT; ADPBT;  
 KW antibody-dependent enzyme mediated prodrug therapy; cytostatic.  
 XX

OS Homo sapiens.  
 XX  
 FN US2003027162-A1.  
 XX  
 PD 06-FEB-2003.  
 XX  
 PF 15-NOV-2001; 2001US-0997428.  
 XX  
 PR 05-NOV-1997; 97MO-US20069.  
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 PR 17-SEP-1998; 98MO-US19437.  
 PR 07-OCT-1998; 98MO-US21411.  
 PR 01-DEC-1998; 98MO-US25108.  
 PR 05-JAN-1999; 99MO-US00106.  
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 QY 61 CysThrArgArgGlyLeuSerGlnValProGlnGlyIleProSerAsnThrArgTyrLeu 80  
 Db 237 TGCACGGCGCGGGCCTCTCCGAGGTCCCGACGGGTATTCCTCGAACAACCCGGTACTC 296  
 QY 81 AsnLeuMetGlnAsnAniIleGlnMetIleGlnAlaAspThrPheArgHisLeuHis 100  
 Db 297 AACCTCATGAGAACACATCCAGATATCAGGCCACACTTCCGCCACCTCCACAC 356  
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Qy      |||
141 GYAlaPheGluTrpLeuSerLeuLeuArgGluLeuTrpLeuArgAsnProIleGlu 160
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RESULT 12

ABX81157 standard; DNA; 2185 BP.

ABX81157;

22-Apr-2003 (first entry)

Novel human secreted or transmembrane protein PRO1344 DNA.

Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing; cardiac insufficiency disorder; cancer; tumour; immune response; adrenal cortical capillary disorder; endothelial growth; c-fos induction; vascular endothelial growth factor inhibition; VEGF inhibition; endothelial cell growth inhibitor; T-lymphocytes stimulation; retinal neurons cell survival; rod photoreceptor cell survival; retinal disorder; retinitis pigmentosa; kidney disorder; mammalian kidney mesangial cell proliferation; Berger disease; dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation; chondrocyte redifferentiation; sports injury; arthritis; gene; ds.

Homo sapiens.

US2003027985-A1.

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14-NOV-2001; 2001US-0990562.

05-NOV-1997; 97WO-US20069.

16-SEP-1998; 98WO-US19330.

17-SEP-1998; 98WO-US19437.

07-OCT-1998; 98WO-US21141.

01-DEC-1998; 98WO-US25108.

05-JAN-1999; 99WO-US00106.

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Gaps:        0

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Val1Cys	Ser2Cys	Ser3Asn	Gln4Phe	Ser5Ile	Val60
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Val1Pro	Gln1Gly	Ile2Pro	Ser3Thr	Arg4Tyr	Leu80
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Met1Leu	Ala1Ala	Ser2Phe	Arg3Ile	Met4His	His100
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Asn5Ser	Ile6Arg	Gln11Leu	Gly12Ala	Phe13Asn	120
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Glu1Leu	Phe2Asp	Ser3Asn	Thr4Phe	Thr5Ile	Pro6Ser
GAGACGCTTTCG	CACACTGCGTGCACGTCATCTCC	476			
Leu9Arg	Glu10Leu	Thr11Phe	Arg12Asn	Pro13Leu	166
CTGGCGGAGCTCG	GCTTCGCAACACCCCATGAA	536			
Arg1Val	Pro2Ser	Leu3Met	Arg4Leu	Asp5Gly	Gln180
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Qy	381	SerVallySTTPLeuLeuProAasnGIYrThrValIIeSerShIsaIAsErArgHIsPArArg	400
Db	1197	TCCGGAAGTGGTGTCTGCCCAATGGAGGACAGTCTACGACAGCCCTCCGCCCAAGG	1256
Qy	401	IIeSerValIIeAasnAspGIYThrLeuAasnPheSerHIsValLeuLeuSerAerAPThrGIY	420
Db	1257	ATCTGTGCTCTCAACAGCGGCACTTTGAACCTTTCCCAAGTGTGTCTTTCAGACACTGGG	1316
Qy	421	ValIYrThrCYMeGCIYThraAsnValAlagIYAasnSerAsnAlaserAlaryrLeuAasn	440
Db	1317	GTGTACATGATGATGTGACCAATGTGTGACGGCAACTCCAAAGCCCTCGGCTCACTCAAT	1376
Qy	441	GIYSerThrAlagIuLeuAasnThrSerAenIYrSerPhePheThrArgIYrThrGIYglu	460
Db	1377	GTGACACAGCGCTGACCTTAACCTCCCACTCAAGCTTCTTCAACACAGTAACAGTGGAG	1436
Qy	461	ThraThrGIUIIeSerProGIUAspThrThraArgIYrLYsPheProValProThrThrSer	480
Db	1437	ACCAAGGAGATTCCTGGCTGAGGACACACAGCGAAGTACAAAGCTTCTCTACACAGTCC	1496
Qy	481	ThrgIYrYrGINProAlATYrThrThrSerThrValLeuIIegInThrThraArgVal	500
Db	1497	ACTGTTATCCAGCGGCATATATACCACTCTACACAGGTGTCTATTCAGACTACCCGGTGG	1556
Qy	501	ProLYsGINValAlaValAProAlaThrAspThrThrAspLYsMeCInThrSerSerLeuAsp	520
Db	1557	CCCAAGCAGGTGGCAGTACCCCGGACAGCACACACTGACGAAGAATGGAGACACACCTGGAT	1616
Qy	521	GIUValMeLylYrThrThrYsIleIleIIegIYCYsPheValAlaValThrlLeuLeuAla	540
Db	1617	GAACTCATGAAGACCAACCAAGATCATCATTTGGCTGTGTGGCACTGACTCTGGTACGT	1676
Qy	541	AlaAlaMeCLeuIleValPheYrLYsLeuAArgLYsArgHIsGINglInArgSerThrVal	560
Db	1677	GCCGCCAATGTTGATTGTCTTATTAACCTTGTAAAGCGGCAACAGCAGCGGAGTACAGTC	1736
Qy	561	ThraIlaaIaArgThrValGIuIleIIegInValAspGIUAspIleProAlaAlaThrSer	580

Db 1737 ACACGCCCGGAGCTGTGATATATCCAGGTGACGACGACATCCGACGACACATCC 1796  
Qy 581 AAlaAlaAlaThraAlaAlaProSerGlyValSerGlyGluGlyAlaValAlaValProThr 600  
Db 1797 GCAGCGACCAACAGACAGCTCCGTCGGTGTATCAGTGAAGGGGCGAGTGTGCTGCCACA 1856  
Qy 601 ILeHisAspHisIleAsnTyrAsnThrTyrLysProAlaHisGlyAlaHisIleProThrGlu 620  
Db 1857 ATTCATGACCATATTAATTAACAACACCTACCAACACGACATGGGGCCCACTGGACAGAA 1916  
Qy 621 AsnSerLeuGlyLysSerLeuHisProThrValThrThrIleSerGluProTyrIleIle 640  
Db 1917 AACAGCGTCGGGAACTCTTCGACCCGACAGTCAACCACTATCTGTAACTTATATATT 1976  
Qy 641 GlnThrHisThrLysAspLysValGlnGluThrGlnIle 653  
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RESULT 13  
ID ABX90247 standard; cDNA; 2185 BP.  
XX ABX90247;  
AC ABX90247;  
XX 01-MAY-2003 (first entry)  
DT  
DE Human secreted/transmembrane protein cDNA, #93.  
XX  
XX Human; gene; ss; PRO; secreted; transmembrane; signal peptide;  
KW pharmaceutical; diagnostic; therapeutic; gene therapy.  
XX  
XX Homo sapiens.  
XX PN US2002160384-A1.  
XX 31-OCT-2002.  
PD  
PF 14-NOV-2001; 2001US-0992598.  
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XX 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
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PR 15-SEP-1999; 99WO-US21090.  
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PR 05-JAN-2000; 2000WO-US00219.  
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PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
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PR 04-JUN-1998; 98US-088021P.  
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PR 10-JUN-1998; 98US-088734P.  
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PR 17-JUN-1998; 98US-089596P.  
PR 17-JUN-1998; 98US-089599P.  
PR 17-JUN-1998; 98US-089600P.  
PR 17-JUN-1998; 98US-089653P.  
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(GERTH ) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Botstein D, Deenoyers L, Eaton DL,  
XX Ferrera N, Fong S, Gerber H, Gertlisen ME, Goddard A, Godowski PJ,  
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF,  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
XX Zhang Z;

DR WPI; 2003-288106/28.  
DR P-PSDB; AB060341.

PT New transmembrane polypeptides and nucleic acids encoding the  
XX polypeptides, useful in gene therapy, in chromosome identification, as

PT chromosome markers, or in generating probes -  
XX  
XX Claim 2; Fig 156; 650pp; English.  
CC The invention discloses isolated PRO secreted/transmembrane polypeptides  
CC comprising a sequence without signal peptide and the nucleic acid  
CC encoding them. The polypeptides can be used to raise antibodies that  
CC specifically bind to the PRO polypeptide, for linking a bioactive  
CC molecule to a cell expressing a PRO protein and for modulating at least  
CC one biological activity of a cell. The PRO polypeptides or  
CC polynucleotides are also useful in gene therapy, in chromosome  
CC identification, as chromosome markers, or in generating probes. The PRO  
CC polypeptides are useful as molecular markers for protein  
CC electrophoresis, and the isolated nucleic acids may be used for  
CC recombinantly expressing those markers. The PRO polypeptides and nucleic  
CC acids may also be used in tissue typing. Anti-PRO antibodies are useful  
CC in diagnostic assays for PRO, and in affinity purification of PRO from  
CC recombinant cell culture or natural sources. The sequences presented in  
CC ABX90083-ABX90468 are the genes encoding, the primers amplifying and the  
CC probes detecting the PRO polynucleotides of the invention.  
CC Note: The sequence data for this patent is also available in electronic  
CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
XX  
SQ Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;

## Alignment Scores:

Pred. No.:	6.73e-284	Length:	2185
Score:	3407.00	Matches:	648
Percent Similarity:	99.39%	Conservative:	1
Best Local Similarity:	99.23%	Mismatches:	4
Query Match:	98.87%	Indels:	0
DB:	25	Gaps:	0

US-09-991-053-10 (1-653) X ABX90247 (1-2185)

QY 1 MetlyseuleuTTPGlnValThrValHisHisThrTPAanaIleleuleuPro 20  
Db 57 ATGAAGCTCTGTGGCAGATGATGTGACACACACCTGGAATGCATCTGCTCCG 116  
QY 21 PheValTyrleuThrAlaGlnValTropileuCyasaIleleuAlaAlaSer 40  
Db 117 TTCGTACTACCTCAGCGCCGCAAGTGTGATCTGTGTGAGCATCTGCTGCGCTCA 176  
QY 41 AlaGlyProGlnAsnCyProSerValCySerCySerAsnGlnPheSerIleVal 60  
Db 177 GCCGGGCCCAAGATGCCCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 236  
QY 61 CysThrArgArgGlyLeuSerGlyValProGlnGlyIleProSerAsnThrArgTyrleu 80  
Db 237 TGCAAGCGCCGCGGCTCTCCGAGGTCCGCGAGGTATTCCTCGAACAACCGGTACTC 296  
QY 81 AsnleuMetGluAsnAsnIleGlnMetIleGlnAlaAspThrPheArgHisleuHis 100  
Db 297 AACCTCATGAGAACCAATCATGATCCAGGCGCACCTTCCGCACTCCACAC 356  
QY 101 LeuGluValleuGlnleuGlyArgAsnSerIleArgGlnIleGluValAlaPheAsn 120  
Db 357 CTGAGAGCTCTGCACTTGGCAGAACTCCATCCGCAATGAGGTGGGGCTTCAAC 416  
QY 121 GlyLeuAlaSerLeuSerThrleuGluLeuPheAsnAsnIlePheThrValIleProSer 140  
Db 417 GGCCTGGCCAGCCTCAACACCTGAGCTGTTCGACCACTGGCTGACATCCCTGAC 476  
QY 141 GlyAlaPheGlyTyrleuSerIleleuArgGluLeuThrPheAsnAsnProIleGlu 160  
Db 477 GGGGCTTTGATATCTCTCAAGCTGGGGAGCTGTGCTTCGCAACACCCCACTCAA 536  
QY 161 SerIleProSerTyrAlaPheAsnArgValProSerLeuMetArgLeuAspLeuGly 180  
Db 537 AGCATCCCTCTTACGCTTCAACCGGAGTCCCTCTCTCATGCGCTGAGCTTGGGGAG 596  
QY 181 LeuIleValleuGluTyrIleSerGlnGlyAlaPheGlnGlyLeuPheAsnleuIleTyr 200

Db 597 CTCAAGAAGCTGAGTATATCTCTGAGGAGCTTTTGAGGGGCTTTCAACCTCAAGTAT 656  
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Db 657 CTGAATTTGGGATGTCCAACTTAAAGACATGCCAATCTCAACCCCCCTGGTGGGCTG 716  
QY 221 GluGluLeuGluMetSerGlyAsnHisPheProGluIleArgProGlySerPheHisGly 240  
Db 717 GAGAGCTGGAGATGAGGGAACCACTTCCCTAGATCAAGGCTGCTCTTCAATGAGC 776  
QY 241 LeuSerSerleuIleValleuThrValMetAsnSerGlnValSerleuIleGluArgAsn 260  
Db 777 CTGAGCTCCCTCAAGAACTCTGGGTATGAACCTCAAGGCTCAAGCTTATGACCGAAT 836  
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Db 897 TTGCCCATGACCTTTACCCCGCTAGGTAAGTGGAGTTCATCAACACACAC 956  
QY 301 ProThrAsnCyAspCyAspIleleuThrleuAlaThrThrleuArgGlyTyrIlePro 320  
Db 957 CTTTGAACCTGTGATTTGTGACATTTGTGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCT 1016  
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QY 341 ValGluValAspGlnAlaSerPheGlnCysSerAlaProPheIleMetAspAlaProArg 360  
Db 1077 GTGAGAGGAGACAGGCTCTCTTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1136  
QY 361 AspleuAsnIleSerGluGlyArgMetAlaGluLeuIleCysAspGlyThrProPheMetSer 380  
Db 1137 GACCTCAACATTTCTGTGAGGCTGATGAGCAAGATTAAGTGTCCGATCCCTCATATGCC 1196  
QY 381 SerValIleThrleuLeuProAsnGlyThrValleuSerHisAlaSerArgHisProArg 400  
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QY 401 IleSerValleuAsnAspGlyThrleuAsnPheSerHisValleuLeuSerAspThrGly 420  
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QY 421 ValIleThrCysMetGlyThrAsnValAlaGlyAsnSerAsnAlaSerAlaTyrleuAsn 440  
Db 1317 GTGTACACATGACATGATGACCAATGTGACAGGCAACTCAACGCTGCTTACTCAAT 1376  
QY 441 GlySerThrAlaGluLeuAsnThrSerAsnTyrSerPhePheThrThrGlyGly 460  
Db 1377 GTGAGACGCTGTGCTTAACTCCCACTCAAGCTTCTTCAACACAGTAACGTGAG 1436  
QY 461 ThrThrGluIleSerProGluAspThrThrArgIleTyrIleAspProValProThrThrSer 480  
Db 1437 ACCAGAGAGATCTGCTGAGGACACACAGGAAAGTACAAGCTGTTCTCAACACGCTCC 1496  
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Db 1557 CCCAAGAGGTGGAGTACCCGCGACAGACCACTGACCAAGATGACAGACAGCTGAGAT 1616  
QY 521 GluValMetIleThrThrIleIleIleGlyCysPheValAlaValThrleuLeuAla 540  
Db 1617 GAATCATGAAGACACACAGATCATCTGCTGCTTGTGGAGTGAAGCTCTGCTGACT 1676  
QY 541 AlaAlaMetleuIleValPheTyrIleleuArgIleArgHisGlnGlnIleAspSerThrVal 560  
Db 1677 GCCGCATGTTGATTTCTTATAAATCTGTAAAGCGGACACGACGAGGAGTACAGTCC 1736



QY 561 ThrAlaAlaArgThrValGluIleIleGlnValAspGluAspIleProAlaAlaThrSer 580  
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Db 1797 GCAGCAGCAACAGAGCTCCGTCGGTGTATCAGGTAGGGGCGCATGAGTCCACCA 1856  
QY 601 IlleHisAspHisIleAsnTyrAsnThrTyrLysProAlaHisIleTyrThrGlu 620  
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QY 621 AsnSerLeuGlyAsnSerLeuHisProThrValThrIleSerGluProTyrIleIle 640  
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QY 641 GlnThrHisThrLysAspLysValGlnGluThrGlnIle 653  
Db 1977 CAGACCATACCAAGACAGATACAGAACTCAATA 2015  
Db 1977 CAGACCATACCAAGACAGATACAGAACTCAATA 2015  
RESULT 14  
ABX77858  
ID ABX77858 standard; cDNA; 2185 BP.  
XX  
AC ABX77858;  
XX  
DT 14-APR-2003 (first entry)  
XX  
DE Human PRO polynucleotide #64.  
XX  
KM Human; PRO; gene; ss; cytosolic; tumour; cancer; breast; lung; stomach;  
KM liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADPPT;  
KM antibody-dependent enzyme mediated produg therapy.  
OS Homo sapiens.  
XX  
PN US2003027163-A1.  
XX  
PD 06-FEB-2003.  
XX  
PF 15-NOV-2001; 2001US-0997666.  
XX  
XX 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
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PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
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PR 16-DEC-1999; 99WO-US30095.  
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PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
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PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
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PR 20-MAR-2000; 2000WO-US07377.  
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PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
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PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
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PR 11-JUN-1998; 98US-088876P.  
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PR 16-JUN-1998; 98US-089440P.  
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PR 22-JUN-1998; 98US-090246P.  
PR 22-JUN-1998; 98US-090252P.  
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PR 24-JUN-1998; 98US-090445P.  
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PR 02-JUL-1998; 98US-091519P.  
PR 02-JUL-1998; 98US-091626P.  
PR 02-JUL-1998; 98US-091628P.  
PR 02-JUL-1998; 98US-091633P.  
PR 02-JUL-1998; 98US-091646P.  
PR 02-JUL-1998; 98US-091673P.  
PR 07-JUL-1998; 98US-091978P.  
PR 07-JUL-1998; 98US-091982P.  
PR 09-JUL-1998; 98US-092182P.  
PR 10-JUL-1998; 98US-092472P.  
PR 20-JUL-1998; 98US-093339P.  
PR 30-JUL-1998; 98US-094651P.  
PR 04-AUG-1998; 98US-095282P.  
PR 04-AUG-1998; 98US-095285P.  
PR 04-AUG-1998; 98US-095301P.  
PR 04-AUG-1998; 98US-095302P.  
PR 04-AUG-1998; 98US-095318P.  
PR 04-AUG-1998; 98US-095321P.  
PR 04-AUG-1998; 98US-095325P.  
PR 10-AUG-1998; 98US-095916P.  
PR 10-AUG-1998; 98US-095929P.  
PR 10-AUG-1998; 98US-096012P.  
PR 11-AUG-1998; 98US-096143P.  
PR 11-AUG-1998; 98US-096146P.  
PR 12-AUG-1998; 98US-096329P.  
PR 17-AUG-1998; 98US-096757P.  
PR 17-AUG-1998; 98US-096766P.  
PR 17-AUG-1998; 98US-096773P.  
PR 17-AUG-1998; 98US-096791P.  
PR 17-AUG-1998; 98US-096867P.  
PR 17-AUG-1998; 98US-096891P.  
PR 17-AUG-1998; 98US-096894P.  
PR 17-AUG-1998; 98US-096895P.  
PR 17-AUG-1998; 98US-096897P.  
PR 18-AUG-1998; 98US-096949P.  
PR 18-AUG-1998; 98US-096950P.  
PR 18-AUG-1998; 98US-096959P.  
PR 18-AUG-1998; 98US-096960P.  
PR 18-AUG-1998; 98US-097022P.  
PR 19-AUG-1998; 98US-097141P.  
PR 20-AUG-1998; 98US-097218P.  
PR 24-AUG-1998; 98US-09761P.  
PR 26-AUG-1998; 98US-097952P.  
PR 26-AUG-1998; 98US-097954P.  
PR 26-AUG-1998; 98US-097955P.  
PR 26-AUG-1998; 98US-097971P.  
PR 26-AUG-1998; 98US-097974P.  
PR 26-AUG-1998; 98US-097978P.  
PR 26-AUG-1998; 98US-097979P.  
PR 26-AUG-1998; 98US-097986P.  
PR 31-AUG-1998; 98US-098014P.  
PR 31-AUG-1998; 98US-098525P.  
PR 16-SEP-1998; 98US-100634P.  
PR 17-SEP-1998; 98US-100858P.

PR 22-DEC-1998; 98US-113296P.  
PR 12-MAR-1999; 99US-123957P.  
PR 23-JUN-1999; 99US-141037P.  
PR 07-JUL-1999; 99US-143048P.

## Alignment Scores:

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Percent Similarity: 99.3% Conservative: 1  
Best Local Similarity: 99.23% Mismatches: 4  
Query Match: 98.87% Indels: 0  
Gaps: 0

US-09-991-053-10 (1-653) x ABX77858 (1-2185)

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QY 21 PheValTyrLeuThrAlaGlnValTyrIleuCyAlaIleAlaIleAlaSer 40  
DB 117 TTCCTTACCTCAGCGGCGCAAGTGTGATCTGTGTGACGCATCGCTGCCCTCA 176  
QY 41 AlaGlyProGlnAsnCyProSerValCysSerCysSerAngInPheSerValVal 60  
DB 177 GCCGGCCCAAGAACTGCCCTCCGTTGCTGTCAGTAACCAAGTTCAGCAAGTGTG 236  
QY 61 CyeThrArgArgGlyLeuSerGluValProGlnGlyIleProSerAsnThrArgTyrLeu 80  
DB 237 TGCACGGCGCGGGCGCTCTCCGAGGTCCCGAGGATTCCTCTGAAACACCCGGTACTC 296  
QY 81 AsnLeuMetGluAsnAsnIleGlnMetIleGlnAlaSerThrPheArgHisIleHis 100  
DB 297 AACCTCATGAGAAACAATCCAGATATCCAGGCCAACACTTCCGCCACTCCACCAC 356  
QY 101 LeuGluValLeuGlnLeuGlyArgAsnSerIleArgGlnIleGluValGlyAlaPheAsn 120  
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DB 477 GGGGCTTTGAATCTCTGCTCAAGCTCGGAGCTCTGCTCCCAACCAACCCATGAA 536  
QY 161 SerIleProSerTyrAlaPheAsnArgValProSerLeuMetArgLeuAspLeuGlyGlu 180  
DB 537 AGCATCCCTCTTACGCTTCAACCGGAGTGCCTCCCTCATGCGCTGACTGGGGAG 596  
QY 181 LeuIleValLeuGluTyrIleSerGluGlyAlaPheGluGlyLeuPheAsnLeuTyr 200  
DB 597 CTCAAGAGCTGAGATATCTCTGAGGAGAGCTTTTAAAGGGCTGTTCACCTCAAGTAT 656  
QY 201 LeuAsnLeuGlyMetCysAsnIleLeuAspMetProAsnLeuThrProLeuValGlyLeu 220  
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QY 221 GluGluLeuGluMetSerGlyAsnHisPheProGluIleArgProGlySerPheHisGly 240  
DB 717 GAGGAGCTGAGAGATGACGGAACCACTTCCCTAGATCAAGGCTGCTCTTCATGCGC 776  
QY 241 LeuSerSerLeuIleValLeuThrValIleMetAsnSerGlnValSerLeuIleGluArgAsn 260  
DB 777 CTGAGCTCCCTCAAGAGCTCTGGGTGATGAATCAACAGGTCACCTGATGACCGGAT 836  
QY 261 AlaPheAspGlyLeuAlaSerLeuValGluLeuAsnLeuAlaHisAsnAsnLeuSerSer 280  
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PR 07-MAY-1998; 98US-084600P.  
 PR 28-MAY-1998; 98US-087106P.  
 PR 02-JUN-1998; 98US-087607P.  
 PR 02-JUN-1998; 98US-087609P.  
 PR 02-JUN-1998; 98US-087759P.  
 PR 03-JUN-1998; 98US-087827P.  
 PR 04-JUN-1998; 98US-088021P.  
 PR 04-JUN-1998; 98US-088025P.  
 PR 04-JUN-1998; 98US-088026P.  
 PR 04-JUN-1998; 98US-088028P.  
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 PR 04-JUN-1998; 98US-088030P.  
 PR 04-JUN-1998; 98US-088033P.  
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 PR 05-JUN-1998; 98US-088202P.  
 PR 05-JUN-1998; 98US-088212P.  
 PR 05-JUN-1998; 98US-088217P.  
 PR 09-JUN-1998; 98US-088655P.  
 PR 10-JUN-1998; 98US-088734P.  
 PR 10-JUN-1998; 98US-088738P.  
 PR 10-JUN-1998; 98US-088742P.  
 PR 10-JUN-1998; 98US-088810P.  
 PR 10-JUN-1998; 98US-088824P.  
 PR 10-JUN-1998; 98US-088826P.  
 PR 11-JUN-1998; 98US-088858P.  
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 PR 12-JUN-1998; 98US-089105P.  
 PR 16-JUN-1998; 98US-089440P.  
 PR 16-JUN-1998; 98US-089512P.  
 PR 16-JUN-1998; 98US-089514P.  
 PR 17-JUN-1998; 98US-089532P.  
 PR 17-JUN-1998; 98US-089538P.  
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 PR 18-JUN-1998; 98US-089801P.  
 PR 18-JUN-1998; 98US-089807P.  
 PR 18-JUN-1998; 98US-089908P.  
 PR 28-AUG-2001; 2001US-0941992.  
 (GETH ) GENENTECH INC.  
 PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Pettrata N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Kijavini IU, Napier MA, Pan J, Paoni NF;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
 PI Zhang Z;  
 XX WPI: 2003-155950/15.  
 DR P-PSDB; ABUS8963.  
 XX New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184,  
 PT PRO361 or PRO646) useful as targets for therapeutic intervention in  
 PT cancers (e.g. lung or breast cancers), or for diagnosing these cancers  
 PT  
 XX Claim 2; Fig 156; 647pp; English.  
 PS  
 XX The invention discloses isolated PRO secreted/transmembrane polypeptides  
 CC comprising a sequence without signal peptide and the nucleic acid  
 CC encoding them. The polypeptides can be used to raise antibodies that  
 CC specifically bind to the PRO polypeptide, for linking a bioactive  
 CC molecule to a cell expressing a PRO protein and for modulating at least  
 CC one biological activity of a cell. The PRO polypeptides or  
 CC polynucleotides are also useful as pharmaceuticals, diagnostics,  
 CC biosensors or bioreactors, for detecting or treating e.g. tumours in  
 CC mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or  
 CC rabbits as targets for therapeutic intervention in certain cancers (e.g.  
 CC colon, lung or breast cancers) and diagnostic determination of the  
 CC presence of these cancers. The PRO polypeptides are also useful as

CC molecular weight markers or for chromosome identification. The PRO genes  
 CC are useful as hybridisation probes or for screening libraries of human  
 CC cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene  
 CC therapy, particularly for replacing a defective gene. The sequences  
 CC presented in ABX79230-ABX79675 are the genes encoding, the primers  
 CC amplifying and the probes detecting the PRO polynucleotides of the  
 CC invention.  
 CC Note: The sequence data for this patent is also available in electronic  
 CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
 XX  
 SQ Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;  
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 Score: 3407.00 Matches: 648  
 Percent Similarity: 99.39% Conservative: 1  
 Best Local Similarity: 99.23% Mismatches: 4  
 Query Match: 98.87% Indels: 0  
 DB: 25 Gaps: 0  
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 QY 21 PheValTyrLeuThrAlaGlnValTrrPileuCyValAlaAlaAlaAlaSer 40  
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 Db 357 CTGAGGCTCCGCACTTGGGAGAGACTCCATCCGAGATGAGTGGGGCTTCAAC 416  
 QY 121 GlyLeuAlaSerLeuSerThrLeuGluLeuPheAspThrPleuThrValIleProSer 140  
 Db 417 GGCCTGCCAGCTTCAACACCTCGAGCTGTTCGACAACTGGCTGACAGCATCTTACGC 476  
 QY 141 GlyAlaPheGluTyrLeuSerTyrLeuArgGluLeuTrrPleuArgAenAnProIleGlu 160  
 Db 477 GGGGCTTTGAATACCTGTCACAGCTGGAGCTTGGCTTCCACACACCCATCGAA 536  
 QY 161 SerIleProSerTyrAlaPheAsnArgValProSerLeuMetArgLeuAspLeuGlyGlu 180  
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 QY 181 LeuLysLeuLeuGluTyrIleSerGluGlyAlaPheGluGlyLeuPheAsnLeuTyr 200  
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 Db 777 CTGAGCTCCCTCAAGAGCTGTGGTCAATGAACTCAAGGTCACTGATGAGCGGAT 836

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 Db 1437 ACCCAGGAGATCTGCTGAGAGACAAACGGAAGTACAAAGCTGTCTTCAACCAAGTCC 1496  
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 QY 601 IleHisAspHisIleAsnTyrAsnThrTyrIleYsProAlaHisGlyAlaHisTyrThrGlu 620  
 Db 1857 ATTCAATGACCATATTAACTACAAACCTTAACAAACGACATGGGGCCCACTGGACAGAA 1916

QY 621 AsnSerLeuGlyAsnSerLeuHisProThrValThrThrIleSerGluProTyrIleIle 640  
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 QY 641 GlnThrHisThrIysAspIysValGlnGluThrGlnIle 653  
 Db 1977 CAGACCATACCAAGGACAAAGTACAGGAAATCAATAA 2015

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 22, 2004, 22:41:41 ; Search time 102 Seconds  
(without alignments)  
2825.718 Million cell updates/sec

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Perfect score: 3446  
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Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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Database : Issued Patents NA.\*

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6: /cgn2\_6/ptodata/2/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3407	98.9	2185	4 US-09-996-243-228	Sequence 520, App
2	1832	53.2	2905	4 US-09-996-243-500	Sequence 13, App
3	988.5	29.0	973	4 US-09-482-273-13	Sequence 13, App
4	977.5	28.4	984	4 US-09-482-273-82	Sequence 82, App
5	425.5	12.3	4843	3 US-08-986-485-1	Sequence 51, App
6	418.5	12.1	2768	4 US-09-996-243-51	Sequence 1, App
7	418.5	12.1	2852	3 US-09-063-950-1	Sequence 1, App
8	416	12.1	2019	3 US-09-063-950-3	Sequence 3, App
9	407	11.6	2461	4 US-09-620-312D-350	Sequence 350, App
10	402.5	11.7	2296	3 US-09-188-930-228	Sequence 228, App
11	402.5	11.7	2296	4 US-09-312-283C-228	Sequence 228, App
12	400	11.6	6814	4 US-09-484-970B-66	Sequence 66, App

13	399.5	11.6	2290	3 US-09-131-648-4	Sequence 4, App
14	399	11.6	4758	3 US-09-191-647-1	Sequence 1, App
15	399	11.6	4758	3 US-09-540-245A-1	Sequence 1, App
16	399	11.6	4758	3 US-09-540-153-1	Sequence 1, App
17	392	11.4	5583	4 US-09-312-283C-372	Sequence 372, App
18	391	11.3	5176	4 US-09-182-024A-1	Sequence 1, App
19	387	11.2	2818	4 US-09-620-312D-92	Sequence 92, App
20	374	10.9	8378	5 PCT-US91-09055-1	Sequence 1, App
21	367.5	10.7	1777	4 US-09-461-325-40	Sequence 40, App
22	309.5	9.0	2734	4 US-09-170-496D-263	Sequence 263, App
23	309.5	9.0	2724	4 US-09-170-496D-277	Sequence 277, App
24	308.5	9.0	7452	3 US-08-592-500-1	Sequence 1, App
25	308.5	9.0	7452	3 US-08-195-006-1	Sequence 1, App
26	308.5	9.0	7452	5 PCT-US94-07644A-1	Sequence 1, App
27	307.5	8.9	1002	1 US-08-442-063A-26	Sequence 26, App
28	307.5	8.9	1026	1 US-08-272-919-1	Sequence 1, App
29	307.5	8.9	1026	1 US-08-619-816-1	Sequence 1, App
30	307.5	8.9	1026	5 PCT-US95-08542-1	Sequence 1, App
31	307.5	8.9	14167	4 US-09-169-768-12	Sequence 12, App
32	303.5	8.8	849	4 US-08-442-063A-44	Sequence 44, App
33	303.5	8.8	924	1 US-08-442-063A-47	Sequence 47, App
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35	287	8.3	4104	4 US-09-996-243-277	Sequence 277, App
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42	241.5	7.0	2612	4 US-09-495-050A-214	Sequence 214, App
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44	238	6.9	1858	2 US-08-286-846A-7	Sequence 7, App
45	238	6.9	1858	2 US-08-457-880A-7	Sequence 7, App

#### ALIGNMENTS

RESULT 1  
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Sequence 228, Application US/09996243  
Patent No. 6478825  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
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APPLICANT: Gottlieb, Mary E.  
APPLICANT: Goddard, Audrey  
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APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secured and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C13  
CURRENT APPLICATION NUMBER: US/09/996, 243  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16





/ PRIOR APPLICATION NUMBER: 60/090863  
 / PRIOR FILING DATE: 1998-06-26  
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 / PRIOR FILING DATE: 1998-07-01  
 / PRIOR APPLICATION NUMBER: 60/091478  
 / PRIOR FILING DATE: 1998-07-02  
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 / PRIOR FILING DATE: 1998-07-02  
 / PRIOR APPLICATION NUMBER: 60/091633  
 / PRIOR FILING DATE: 1998-07-02  
 / PRIOR APPLICATION NUMBER: 60/091978  
 / PRIOR FILING DATE: 1998-07-07  
 / PRIOR APPLICATION NUMBER: 60/091982  
 / PRIOR FILING DATE: 1998-07-07  
 / PRIOR APPLICATION NUMBER: 60/092182  
 / PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.: 0 Length: 2185  
 Score: 3407.00 Matches: 648  
 Percent Similarity: 99.39% Conservative: 1  
 Best Local Similarity: 99.23% Mismatches: 4  
 Query Match: 98.87% Indels: 0  
 DB: 4 Gaps: 0

US-09-991-053-10 (1-653) x US-09-996-243-228 (1-2185)

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 QY 21 PheValTyrLeuThrAlaGlnValTyrPheLeuCysAlaAlaIleAlaAlaSer 40  
 Db 117 TTCGTACTCACTGAGGCGCAAGTGTGATTCTGTGTGACCAATGCTGCTGCGCTCA 176  
 QY 41 AlaGlyProGlnAsnGlyProSerValCysSerCysSerAsnGlnPheSerValVal 60  
 Db 177 GCGGCGCCGAGAACCTGCCCTCGTTGCTGCGGTAACCACTTCACCAAGGTGGTG 236  
 QY 61 CysThrArgArgGlyLeuSerGluValProGlnGlyTyrProSerAsnThrArgTyrLeu 80  
 Db 237 TGAACGCGCGGGGCTCTCCAGAGTCCCGAGGATATTCCTCGAACACCGGATCTC 236  
 QY 81 AsnLeuMetGlnAsnAsnIleGlnMetIleGlnAlaAspThrPheArgHisLeuHisHis 100  
 Db 297 AACCTATGAGAAACAATCCAGATATCCAGGCGGACACTTCGCGCACCTCCACAC 356  
 QY 101 LeuGluValLeuGlnLeuGlyArgAsnSerIleArgGlnIleGluValGlyAlaPheAsn 120  
 Db 357 CTGAGAGTCTCTGAGTTGGGACAGAACTCCATCCGCGAGATGAGTGGGCGCTTCAC 416  
 QY 121 GlyLeuAlaSerLeuSerThrLeuGluLeuPheAspAsnThrLeuThrValIleProSer 140  
 Db 417 GGCCTGCGCCAGCTCAACACCTGAGACTGTGCAACAATGCGTGAGACATCTCCAGC 476  
 QY 141 GlyAlaPheGlyTyrLeuSerTyrLeuArgGlyLeuTyrPheLeuArgAsnAsnProIleGlu 160  
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 QY 161 SerIleProSerTyrAlaPheAsnArgValProSerLeuMetArgLeuAspLeuGlyGlu 180  
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 QY 181 LeuLeuTyrLeuGlyTyrIleSerGluGlyAlaPheGlyGlyLeuPheAsnLeuTyr 200  
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 Db 777 CTGAGCTCTCTCAAGAGCTGTGGGTCAATGAACTCAAGAGTCAAGCTTGAAGCCGAA 836  
 QY 261 AlaPheAspGlyLeuAlaSerLeuValGluLeuAsnLeuAlaHisAsnAsnLeuSerSer 280  
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 QY 321 ThrAsnSerThrCysCysGlyArgCysHisAlaProMetHisMetArgGlyArgTyrLeu 340  
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Qy 601 ILeHisAspHisIleAsnThrTyrAsnThrTyrLysProAlaHisGlyAlaHisTyrThrGlu 620  
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Db 1917 AACAGCTGGGGAATCTCTCCACCCCAAGTCAACCATATCTGAACTTATTAATTT 1976  
Qy 641 GlnThrHisThrLysAspLysValGlnGlnThrGlnIle 653  
Db 1977 CAGACCCATACCAAGACAGAGTACAGAAATCTAAATA 2015  
RESULT 2  
US-09-996-243-500  
Sequence 500, Application US/09996243  
Patent No. 6478825  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
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APPLICANT: Williams, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C13  
CURRENT FILING DATE: US/09/996,243  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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 PRIOR APPLICATION NUMBER: 60/091633  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091978  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
 Pred. No.: 1,44e-189 Length: 2906  
 Score: 1832.00 Matches: 361  
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 Best Local Similarity: 55.97% Mismatches: 138  
 Query Match: 53.16% Indels: 41  
 Gaps: 14

US-09-991-053-10 (1-653) x US-09-996-243-500 (1-2906)

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QY 41 AlaGlyProGlnAsnGlyProSerValCysSerCysSerAsnGlnIleHisLeuVal 60  
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QY 61 CysThrArgArgGlyLeuSerGlyValProGlnGlyIleProSerAsnThrArgTyrLeu 80  
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QY 81 AsnLeuMetGluAsnAsnIleGlnMetIleGlnAlaAspThrPheArgHisLeuHis 100  
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QY 181 LeuLeuLeuArgGluTyrIleSerGluGlyAlaPheGluGlyLeuPheAsnLeuTyr 200  
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 Db 2015 CGGAATGCTGTGCTCAGTATGGTATCGTTAAATTTCACAAAATGTAACTCAAGATACA 2074  
 QY 420 GlyValIYThrCysMetGlyThrArgValIaGlyAnSerAsnAlaSerAlaTrieu 439  
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 QY 440 AsnGlySerThrAlaGluLeuAnSerHisSerAnTYSerPhePheThrThrGly 459  
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 Db 2189 GAGACTATGGAACCGCTCTCAGGATGAGGACACGACCAAGATTAACAATGGGTGCCACT 2248  
 QY 477 Pro-----ThrThSerThrArgLysArgProAlaTYThrThSerThr 491  
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 QY 492 ThrValLeuIleGlnThrThrArg---ValProLysGlnValAlaValProAlaThrAsp 510  
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 QY 591 SerGlyGluGluAlaValaValLeuProThrIle---HisAspHisIleAsn---TyrAsn 608  
 Db 2555 -----GAAAGCCACTGCGCATGCTCTGTATCGAGCATGAGCACTTAAATCATCTAAC 2608  
 QY 609 ThrTYLysProAlaHisGlyAlaHisIleArgThrGluAnSerLeuGlyAnSerLeuHis 628  
 Db 2609 TCATTCAAATCTCCCTTCACACACACAAACAGTAACACATAT--AATTCATATAC 2665  
 QY 629 ProThrValThrThrIleSerGluProTYLysIleIleGlnThrHisThrLysAspLysVal 648  
 Db 2666 -----AGTTCAGTCATGAACGGTATATGATCCGAATGAAGACTCTAAAGACATGTA 2716  
 QY 649 GlnGluThrGlnIle 653  
 Db 2717 CAAGAGACTCAATC 2731

```

? PatentNo: 6534631
? GENERAL INFORMATION:
? APPLICANT: Rosen et al.
? TITLE OF INVENTION: 71 Human Secreted Proteins
? FILE REFERENCE: P2030P1
? CURRENT APPLICATION NUMBER: US/09/482,273
? CURRENT FILING DATE: 2000-01-13
? EARLIER APPLICATION NUMBER: PCT/US99/15849
? EARLIER FILING DATE: 1999-07-14
? EARLIER APPLICATION NUMBER: 60/092,921
? EARLIER FILING DATE: 1998-07-15
? EARLIER APPLICATION NUMBER: 60/092,922
? EARLIER FILING DATE: 1998-07-15
? EARLIER APPLICATION NUMBER: 60/092,956
? EARLIER FILING DATE: 1998-07-15
? NUMBER OF SEQ ID NOS: 267
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 13
? LENGTH: 973
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-482-273-13

```

Alignment Scores:	
Pred. No.:	2.78e-99
Score:	998.50
Percent Similarity:	84.56%
Best local Similarity:	73.75%
Query Match:	28.98%
DB:	4
US-09-991-053-10 (1-653)	x US-09-482-273-13 (1-973)
	Length: 973
	Matches: 191
	Conservative: 28
	Mismatches: 37
	Indels: 3
	Gaps: 1

QY	3	AlaIleAlaAlaAlaAlaSerLeuAlaIle-----ProGlnAmCysProSerValCys	50
Ds	191	GGCGTAAACGCTGGCGCGCGAGAGGGGGCTCCCCCGGCGACCTCTGGCCCGTGGCGCTGC	256
QY	51	SerCysSerAsnGlnPheSerIleValCysThrArgArgGlyLeuSerGluValPro	70
Ds	251	TCCTGGACGACACCAAGGCCAGCGCGGGTGAATCTGCACAGGAGACACTGGCCGAGGTCCA	31.0
QY	71	GlnGlyIleProSerSerThrArgTyrLeuAsnLeuMetGluAsnAsnIleGlnMetIle	90
Ds	311	GCCAGAGATCCCGGTCAACACGCGGTAACTGGAACCTGCACAAAGAAACGCGATCTCAGGTATC	370
QY	91	GlnAlaAspThrPheArgHisLeuHisIleGluValLeuGlnLeuGlyArgAsnSer	110
Ds	371	CGAGACGACACCTTCAAGACCTGGCGGACCTGGAGATTTCTGCACGTGACGAGAACACTTG	430
QY	111	IleArgGlnIleGluValGlyAlaPheAsnGlyLeuAlaSerLeuSerThrLeuGluLeu	130
Ds	431	GTGCGAAGATGGAAGTGGGGCGCTTTCACACGGGCGTCCCACTCAACACGCTGGAGCTT	490
QY	131	PheAspAsnTrpLeuThrValIleProSerGlyAlaPheGlyTyrLeuSerIleValArg	150
Ds	491	TTTGACAAACCGGCTGACCAACGCTGCCCAACGAGGCGTTTCAAGTACCTGTCCAGACTGGCG	550
QY	151	GluLeuTrpLeuArgAsnAsnProIleGluSerIleProSerTyrAlaPheAsnArgVal	170
Ds	551	GAACTCTGGCTGGGAACAACCCATCGAAGACATCCCTCTACGGCTTCAACCGGGTGG	610
QY	171	ProSerLeuMetArgLeuAspLeuGlyGlnLeuValIleValLeuGluTyrIleSerGlnGly	190
Ds	611	CCTTGGCTCGGGGGCTGGACCTGGGCGAAGCTCAAGCGGCTGGAATCATCTCGAGAGCG	670
QY	191	AlaPheGlnGlyLeuPheAsnLeuIleTyrLeuAsnLeuGlyMetCysAsnIleLeuAsp	210
Ds	671	GCCTTGAAGGGGCTGGTCAACTGGCGTCACTCAACCTGGGCAATGCTCAACTCAAGAC	730
QY	211	MetProAsnLeuThrProLeuValGlyLeuGlnGluLeuGluMetSerGlyAsnHisPhe	230
Ds	731	ATCCCAACCTTACAGCCCTGGTGGCTGGACGAGAGCTGGAGAGCTGTGGGGAACCGGCTG	790

QY 231 ProgluileargProglySerPheHISGLYLeuSerSerLeuYblyLeuTPValMet 250  
 Db 791 GACCTGTGGTGGGAACAACCCATCGAGAGCATCCCTCTCAACCCCTTCAACCCGCTG 616  
 QY 251 AsnSerGlnValSerLeuIleGluArgAsnAlaPheAspGlyLeuAlaSerLeuValGlu 190  
 Db 851 CAGCCGAGGTACACCATCGAGCGCAACGCTTTCACAGACCTCAAGTGTGTGAGAGAG 676  
 QY 271 LeuAsnLeuAlaHisAsnAsnLeuSerSerLeuProHisAspLeuPheThrProLeu 210  
 Db 911 CTCACCTGTCCCAACAACCTGATGTCCGTGCCCAACGACCTTTCACGCCCTG 736

## RESULT 4

US-09-482-273-82  
 ; Sequence 82, Application US/09482273  
 ; Patent No. 6534631  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: 71 Human Secreted Proteins  
 ; FILE REFERENCE: P2030P1  
 ; CURRENT APPLICATION NUMBER: US/09/482,273  
 ; CURRENT FILING DATE: 2000-01-13  
 ; EARLIER APPLICATION NUMBER: PCT/US99/15849  
 ; EARLIER FILING DATE: 1999-07-14  
 ; EARLIER APPLICATION NUMBER: 60/092,921  
 ; EARLIER FILING DATE: 1998-07-15  
 ; EARLIER APPLICATION NUMBER: 60/092,922  
 ; EARLIER FILING DATE: 1998-07-15  
 ; EARLIER APPLICATION NUMBER: 60/092,956  
 ; EARLIER FILING DATE: 1998-07-15  
 ; NUMBER OF SEQ ID NOS: 267  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 82  
 ; LENGTH: 984  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-482-273-82

## Alignment Scores:

Pred. No.: 5.6e-97 Length: 984  
 Score: 977.50 Matches: 192  
 Percent Similarity: 83.65% Conservaive: 28  
 Best Local Similarity: 73.00% Mismatches: 40  
 Query Match: 28.37% Indels: 4  
 Gaps: 1

US-09-991-053-10 (1-653) x US-09-482-273-82 (1-984)

QY 34 AlaIleAlaAlaAlaAlaSerAlaGly-----ProGlnAsnCyProSerValCys 50  
 Db 197 GCCCTGACGTCTGCCCGGAGGGGGCTCCCCCGGCGCACCTCTGCTCCCTGCTGCTGC 256  
 QY 51 SerCySerAsnGlnPheSerLeuValValCysThrArgArgGlyLeuSerGluValPro 70  
 Db 257 TCCGACGACCAACGAGCGGCGGCTGATCGACACGAGAGAMCTGCGCAGAGTCCCA 316  
 QY 71 GlnGlyLeuProSerAsnThrArgTyrLeuAsnLeuMetGluAsnAlaIleMetIle 90  
 Db 317 GCCACGATCCCGTCAACACGCGGTACCTGAACCTGCAAGGAAGCGGATCCAGGTATC 376  
 QY 91 GlnAlaAspThrPheArgHisIleuHisIleuGluValLeuGlnLeuGlyArgAsnSer 110  
 Db 377 CGGACGACACGCTTCAAGACCTCGGACCTGAGAGTTCGACGCTGAGCAAGAACCTG 436  
 QY 111 IleArgGlnIleGluValGlyValPheAsnGlyLeuAlaSerLeuSerThrLeuGluLeu 130  
 Db 437 GTGGCGAAGATCGAGTGGGCGCTTCAACGCGCTGCGCAACCTCAACACGCTGAGCTT 496  
 QY 131 PheAspAsnThrLeuThrValIleProSerSerGlyAlaPheGlyTyrLeuSerLeuArg 150  
 Db 497 TTTCACACCGGCTGACACCGGTCCACGAGGCTTGTGAGTACCTGTCCAACTGCGG 556  
 QY 151 GluLeuThrLeuArgAsnAsnProIleGluSerIleProSerTyrAlaPheAsnArgVal 170

Db 557 GACCTGTGGTGGGAACAACCCATCGAGAGCATCCCTCTCAACCCCTTCAACCCGCTG 616  
 QY 171 ProSerLeuMetArgLeuAspLeuGlyIleuValLeuGluTyrIleSerGluGly 190  
 Db 617 CCTCTGCTGGGGCTGTGACCTGGGCGAGCTCAACGCGCTGGAATACATCTCGAGGGG 676  
 QY 191 AlaPheGluGlyLeuPheAsnLeuIleTyrTyrLeuAsnLeuGlyMetCysAsnIleIleAsp 210  
 Db 677 GCCTTGAGGGGTGTGTAACCTGCGCTACCTCACTGGGATGTGCAACCTCAAGGAGC 736  
 QY 211 MetProAsnLeuThrProLeuValGlyLeuGluGluLeuGluMetSerGlyAsnHisPhe 230  
 Db 737 ATCCCAACCTG-ACGGCCCTGGTGGCGCTGAGAGACTGAGAGCTGTGTGGGCAACCGGCTG 795  
 QY 231 ProgluileargProglySerPheHISGLYLeuSerSerLeuYblyLeuTPValMet 250  
 Db 796 GACCTGTGGTGGGAACAACCCATCGAGAGCATCCCTCTCAACCCCTTCAACCCGCTG 855  
 QY 251 AsnSerGlnValSerLeuIleGluArgAsnAlaPheAspGlyLeuAlaSerLeuValGlu 270  
 Db 856 CAGCCGAGGTACACCATCGAGCGCAACGCTTTCACAGACCTCAAGTGTGTGAGAGAG 915  
 QY 271 LeuAsnLeuAlaHisAsnAsnLeuSerSerLeuProHisAspLeuPheThrProLeu 290  
 Db 916 CTCACCTGTCCCAACAACCTGATGTCCGTGCCCAACGACCTTTCACGCCCTG 975  
 QY 291 TyrLeuVal 293  
 Db 976 CGCCTCGTA 984

## RESULT 5

US-08-986-485-1  
 ; Sequence 1, Application US/08986485  
 ; Patent No. 6046030  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WU, SHUJIAN  
 ; APPLICANT: SWEET, RAYMOND  
 ; APPLICANT: TRUNEH, ALEMESEGED  
 ; TITLE OF INVENTION: A HUMAN LIG-1 HOMOLOG (HLIG-1)  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: RAYNER & PRESTIA  
 ; STREET: P.O. BOX 980  
 ; CITY: VALLEY FORGE  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19482  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FASTSEQ for windows version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/986,485  
 ; FILING DATE: 08-DEC-1997  
 ; CLASSIFICATION:  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/059,448  
 ; FILING DATE: 22-SEP-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: PRESTIA, PAUL F  
 ; REGISTRATION NUMBER: 23,031  
 ; REFERENCE/DOCKET NUMBER: GH-70264  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 610-407-0700  
 ; TELEFAX: 610-407-0701  
 ; TELEX: 846169  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4843 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-986-485-1

## Alignment Scores:

Pred. No.: 2,11e-35 Length: 4843  
Score: 425.50 Matches: 191  
Percent Similarity: 32.01% Conservative: 99  
Best Local Similarity: 21.08% Mismatches: 269  
Query Match: 12.35% Indels: 347  
DB: 3 Gaps: 30

US-09-991-053-10 (1-653) x US-08-986-485-1 (1-4843)

```

Qy 28 VALTRPLeuCyAlaAla1le---AlaAlaAlaSerAlaGlyProGln---Asn 45
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
85 CTCGTGCGCTTTTCTTCTCGGTGAGCGCGGAGCCGCCGCCGCCGCCGCCGCCGCC
Qy 46 CysProSerValCysSerCysSerAsnGln-----PheSerLysValVal 60
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
145 TGCCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
Qy 61 CysThrArgArgGlyLeuSerGlyValProGlnGlyLeuProSerAsnThrArgTyrLeu 80
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
205 TGCCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
Qy 81 AsnLeuMetGluAsnAsnIleGlnMetIleGlnAlaAspThrPheArgHisLeu----- 98
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
265 AACCTGAGTTACACAAACTCGCTGAGATTGACCTCGCTGTTTGAGACTTGCACGAC 324
Qy 99 -----HisHis----- 100
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
325 CTACAGAAAGTATCCTCATATATCATGATTGACAGCGGTAGCATCACTGCGCGTGTGT 384
Qy 100 ----- 100
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
385 TCATCACAAGTAGTGTCTCTCTTCTTGACAGACACAAATCGACGCTCGACGGAGC 444
Qy 101 -----LeuGluValLeuGlnLeuGlyArgAsnSerIleArgGln 113
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
445 CAGCTGAAGGCTTACTCTCTCTAGAGTGTGATGATCTGAATCTGAACAACTACGGA 504
Qy 114 Ile----- 114
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
505 GTGCGGAACCTACTTCCACACGACCGCTATTAAGAGCTCAACCTGACAGGCAT 564
Qy 115 -----GluValGlyAlaPheAsnGlyLeuAla---SerLeuSerThrLeu 128
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
565 CGGATTGCGACCTGAGAGTGTGAGCATTTGATGTGTCTGACGCGTCTCTACTT 624
Qy 129 GluLeuPheAspAsnTrpLeuThrValIleProSerGlyAlaPheGluTyrLeuSerLys 148
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
625 CGCTGAGCAAAACAGATCAACCAAGCTTCTCTTAAGAGCATTTCAAG---CTACCCAGG 681
Qy 149 LeuArgGluLeuTrpLeuArgAsnAsnProIleGluSerIleProSerTyrAlaPheAsn 168
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
682 CTGACACAACCTGAGCTCAATCGGAACAGATTGCGGTGATAGAGGCGCTCACTTCAG 741
Qy 169 ArgValProSerLeu-----MetArgLeuAspLeuGlyGluLeuLys----- 183
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
742 GGGCTCAACAGCTTGAGAGTGTGTAAGCTTCAGCGAAACAACATGACGAAACTGACAGAT 801
Qy 184 -----LeuGluTyr----- 186
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
802 GGGGCTTCTGGGAGCTGTCCAAAATGCAATGTGTCTGACCTGAGAGTACAGACCTGTGTA 861
Qy 187 ---IleSerGluGlyAlaPheGluGlyLeuPheAsnLeuLysTyrLeuAsnLeuGlyMet 205
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
862 GAGTGAACAGAGCGCTCGCTCAAGGCTCAAGCGGCTGACATCACTCACTCAAGCAAC 921
Qy 206 CysAsnIleLys----- 209
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
922 AATTCATGTGCTGCGATTACCGCAAGGCTGAGCTTCTGCGAAGAGCTCATGATGTG 981

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Qy 210 -----AspMetProAsnLeuThrProLeuValGly 219
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
982 GTCTGTCTTCAACAACCTGACACGCGCTGAGAGAGAGCTGGCCGACGTGAGCAGC 1041
Qy 220 LeuGluGluLeuGluMetSerGlyAsnHisPheProGluIleArgProGlySerPheHis 239
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1042 CTGAGTGTCTGTGCTGCTGACCCACCAATTCATGAGCCACATTCGCGAGGTGCTTCAG 1101
Qy 240 GlyLeuSerSerLeuLys----- 245
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1102 GGACTCAGAGGCTTGGCAGTCTTGATCTGACCATTAACAGATTTGGGACAAATAGAG 1161
Qy 246 -----LysLeuTrpValMetAsn 251
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1162 GACACAGCGCGGCTTCTGAGGCTCGAATTCGGCCACAGCAAGCTGACTGTGTTGGA 1221
Qy 252 SerGlnValSerLeuIleGluArgAsnAlaPheAspGlyLeuAlaSerLeuValGluLeu 271
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1222 AACAAATCAAGTCTGTGCTTAAGAGCATTTCTCGGGCTGGAGAGGCTGAGCACCTG 1281
Qy 272 AsnLeuAlaHisAsnAsnLeuSerSerLeuProHisAspLeuPheThrProLeuArgTyr 291
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1282 AACCTTGAAGGAAATGCGATCAATCTGTCCAGTTGATCCCTTTTGAAAGATGAAGAT 1341
Qy 292 LeuValGluLeuHisLeuHisAsnProTrpAsnCysAspCysAspIleLeuTrpLeu 311
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1342 CTTAAGAGCTCCATATACAGACGACAGCTTCTGTGATCTGACGCGCAAGTGTGCTG 1401
Qy 312 AlaTrpTrpLeuArgGlyTyrIleProThrAsnSerThrCysArgIleArg----- 328
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1402 CCCCCTGGCTTA-----ATGGCAGAGATGCTGACAG 1431
Qy 329 -----CysHisAlaProMetHisMetArgGlyArgTyrLeuValGlu 342
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1432 GCCTTTGTACAGCCACTGTGCCCCACCAAGATCACTGAAGGCTCAGACATTTCTCT 1491
Qy 343 ValAspGlnAlaSerPheGlnCysSer----- 351
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1492 GTGCGACCAAGAGTTTCTGTGTGATGATCTTCTGTAAGCCACAGATCATCCACAGCA 1551
Qy 351 ----- 351
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1552 GAACACCAATGCTATGTGTGGCAGAGACATCCGTTTACATGCTGACGACGACGAGC 1611
Qy 351 ----- 351
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1612 AGCAGTCCCCCATGACCTTGTGCTGAGAGAAAGACATGAAGTCTGACCAATGACAGAC 1671
Qy 351 ----- 351
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1672 ATGAGAACTTTGTCCACGTCCACAGCGCAGAGAGGGAATGATGAGTACACACCATC 1731
Qy 351 ----- 351
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1732 CTGACCTCCGTAGTCACTTTCGGGACAGAGGCGCTAACCAATGTATCATCACCAAC 1791
Qy 352 -----AlaProPheIle 355
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1792 CACTTGGCTTCCACTATTACATTAAGGCGAGGCTCACCTGATGTGTTGCCATTCATTC 1851
Qy 356 MetAspAlaProArgAspLeuAsnIleSerGluGlyArgMetAlaGluLeuLysCysArg 375
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1852 ACCAAACGCCCCACAGCATTAACCATTCGACACACACCGTGGCCGCCCTCGAATGTGCT 1911
Qy 376 ThrPro-----ProMetSerSerValLysTrpLeuLeuProAsnGlyThrValLeuSer 393
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1912 GCACAGAGTACCCAAACCTCAGATGTGCTGGAGAAAGATGAGGACAGCATTTTCCCC 1971
Qy 394 HisAlaSerArgHisProArgIleSerValLeuAsnAspGlyThrLeuAsnPro---Ser 412
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1972 ---GTCGCCGTGAGCAGCAGCATGATCATGATCCGAGTATGACAGCATGTTTTCATCACT 2028

```

Qy 413 HisValLeuSerAspThrGlyValTyrThrCysMetGlyThrAsnValAlaGlyAsn 432  
Db 2029 GATGTGAAATGATGACGAGGGGTTTACAGTGTACTGTACAGACTCAGCGGTTCT 2088  
Qy 433 SerAsnIleSerAlaTyrLeuAsn----- 440  
Db 2089 ATTTCAGCTAATGACCTGACTGTCTAGAGACCCATCCTTGTGTCCCTTGAA 2148  
Qy 441 -----GlySerThrAlaGluLeuAsn-----ThrSerAsn--- 450  
Db 2149 GACCGTGTGATGTGGGAGAAACAGTGCCCTTCAAGCAAGCAAGCGGAGACCT 2208  
Qy 451 -----TyrSerPhePhe-----ThrThrGlyThrGlyThrGlu 463  
Db 2209 CCGCGCCGACCTGCTGTTCAAGGGGACCGCGGTGAGCCTCAGTACGCGGACAC 2268  
Qy 464 IleSerProGluAspThrThrArgLysTyrLysProValProThrThrSerThrGlyTyr 483  
Db 2269 CTGACCCCTGACACGACGCTCTGTGATTCAGAACCTGTGGCAGAGATGCGGCGC--- 2325  
Qy 484 GluProAlaTyrThrThrSerThrThrValLeuIleGlnThrThrArgValProLysGln 503  
Db 2326 -----CGATTTACTGTTGATGTCCAAACCTGGGACGAGGAGCTCAGACGCG 2379  
Qy 504 ValAlaVal-----ProAlaThrAspThrThrAspLysMetGlnThrSerLeuAspGluVal 522  
Db 2380 CTGACGCTCTGCGCGGACGAGCTGACGAGAAAGATGGACACAG----- 2424  
Qy 523 MetLysThrThrLysIleIleIleGlyCysPheVal-----AlaValThr 537  
Db 2425 -----GTAGGATCTTTCACCATGCTGTCTGAGCAGCATGCTC 2463  
Qy 538 LeuLeuAlaAlaAlaMetLeuIleValPheTyrLysLeuArgLysArgLysGlnArg 557  
Db 2464 CTGACGTACCTGCTGGGTGGTGCATCTTACCAACGACGAGAAAGATGAAGAGTAC 2523  
Qy 558 SerThrValThrAlaAlaArgThrValGluIleIleGlnValAspGluAspIleProAla 577  
Db 2524 AGTGTACCAACACAGATGAACCGCTC-----GTGCACACAGATGTTCCAAGC 2571  
Qy 578 AlaThrSerAlaAlaAlaThrAlaAla-----ProSerGlyValSerGlyGluGly 594  
Db 2572 TACCTCTCTCTCAGGGGACCTTCTGACCGACAGAAACCGGTGTGACGAGCGAGGT 2631  
Qy 595 AlaValValLeuProThrIleHisAspHisIleAsnTyrAsnThrTyrLysProAlaHis 614  
Db 2632 GGC-----CCTCAGGCGCAATGGGACATTGAGAGCAATGTTGTGTCCAAGAT 2682  
Qy 615 GlyAlaHisThrGlu 620  
Db 2683 GCAGCCACCTTCCAGAG 2700

RESULT 6  
US-09-996-243-51  
Sequence 51, Application US/09996243  
Patent No. 6478825  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Batton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary B.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gunney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
Pan, James

APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OR INVENTION: Acids Encoding the Same  
FILE REFERENCE: F2730P1C13  
CURRENT APPLICATION NUMBER: US/09/996,243  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087609  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/088025  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088026  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088028  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088029  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088030  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088033  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088326  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088167  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088202  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088212  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088217  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088655  
PRIOR FILING DATE: 1998-06-09  
PRIOR APPLICATION NUMBER: 60/088734  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088738  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088742  
PRIOR FILING DATE: 1998-06-10





QY 141 -----GlyAlaPheGluTyrLeuSerTyrLeuArgGluLeu 152  
 Db 519 AACGCATCCGCCATCATCCAGCTGTGCTTGACACGCTCCAGCGCTCTGAGACTC 578  
 QY 153 TripleArgAsnProIleGluSerTyrAlaPheAsnValProSer 172  
 Db 579 AAGCTGACGACACGAGCTGCGGCGACTGCCCCGCTG-----CGCTGCCCCG 629  
 QY 173 LeuMetArgLeuAspLeuGluGluLeuTyrTyrIleSerGluAlaPhe 192  
 Db 630 CTGCTGCTGTGAGCTGACCTGAGCCAC--AACAGCTCTGCGCCCTGAGCCCGGATCTG 686  
 QY 193 GluGluLeuPheAsnLeuTyrTyrLeuAsnLeuGluMetCysAsnIleTyrAspMetPro 212  
 Db 687 GAC---ACTGCACACGAGAGGCGCTGCGCTGCTGCTGCGGCGCGAGAGCTGAGC 743  
 QY 213 Asn-----LeuThrProLeuValGluLeuGluLeuMetSerGluAsnIlePhe 230  
 Db 744 GAGGGGCTTTCAGCCCTTGCAGACCTCCAGACCTGATGTGTCCAGACACAGCTG 803  
 QY 231 ProGluLeuArgProGlySerPheIleGluLeuSerSerLeuTyrValMet 250  
 Db 804 GAGCGAGTG---CCAGCTGTGATCCGAGGCTCCGAGGCTGAGCGGCTGCGAGCTGAGC 860  
 QY 251 ---AsnSerGluValSerLeuIleGluArgAsnAlaPheArgTyrLeuAlaSerLeuVal 269  
 Db 861 GCGACACACCGCATTCGCCAGCTGCGGCGGAGAGACCTGCGCGGCTGCGCTGAG 920  
 QY 270 GluLeuAsnLeuAlaIleAsnAsnLeuSerSerLeuProIleAsp-----LeuPhe 286  
 Db 921 GAGCTGATGTAGACCACTTAAGCTGACGCTGCTGCTGCGAGCTGCGGCTCTTC 980  
 QY 287 ThrProLeuArgTyrLeuValGluLeuIleMetIleAsnProThrPheCysAspCys 306  
 Db 981 CCCGCTGCGCTGCTGCGAGCTGCC-----CGCAACCTCTTCACCTGAGTGTGC 1031  
 QY 307 AspIleLeuTyrPheAlaTyrTyrLeuArgGlu---TyrIleProThrAsnSerThrCys 325  
 Db 1032 CCCCTGAGCTGTGTTGGCCCTGCGGTGCGAGAGCCAGCTCAACAGCTGAGCCGCTGAG 1091  
 QY 326 CysGluArgCysIleValaProMetIleMetArgGluArgTyrLeuValGluValAspGln 345  
 Db 1092 GAGAGCGCTGCACTTCCGCCCAAGAGAGCTGCGGCTGCTGAGACTTGATAC 1151  
 QY 346 AlaSerPheGlnCysSerAla-ProPheIleMetAspAlaProArgAspLeuAsnIleSe 365  
 Db 1152 GCCGACTTGTGCTGCCAGCCACCA-----CCAGCAGAGCCAGCTGCCAC 1199  
 QY 365 GlnGluArgMetAlaGluLeuTyrCysArgThrProMetSerSerValTyrPhe 385  
 Db 1200 ACGAGGCGCTG-----TGCGGAGGCCACAGCGCTGTCTTTCAGCTTGCT 1247  
 QY 385 uLeuProAsnGluTyrValLeuSer-HisAlaSerArgHis-----ProArgI 401  
 Db 1248 CCTACCTGCGC-----TTAGCCCAACAGCGCGGCACTAGAGGCCCGGAGCCGCGCC 1298  
 QY 401 LeuSerValLeuAsnAspGluTyrLeuAsnPheSerHisValLeuLeuSerAspThrGly 421  
 Db 1299 TCCACTGCCGCCACCGAC----- 1315  
 QY 421 alTyrThrCysMetGluTyrAsnValAla-GlyAsnSerAsnAlaSerAlaTyrLeuAsn 440  
 Db 1316 -----TGAGGCGCTGTGCTCCCAAGCCCAAGACTGCCACCGTTCACCTGCTCAT 1367  
 QY 441 GlySerThrAlaGluLeuAsnThrSerAsnTyr----- 451  
 Db 1368 GGGGGACATGCACTGCGGAGACGAGCAACACCTGCGGTCTGTGCTGCCGAGAGGCTTC 1427  
 QY 452 -----SerPhePheThrThrGluTyrGluTyrThrGluIleSerProGluAspThr 469  
 Db 1428 ACGGCGCTGTACTGTGAGACCAAGATGCGGAGGAGACAGGCCAGCTTACACCAAGTC 1487

QY 470 ThrArgLeuTyrLeuPheProValProThrThrSerThrGluTyrGlnProAlaTyrThr 489  
 Db 1488 ACGCG-----AGGCCACCAACGCTCCAGCTGAGCTGAGGATGAGCGGAGAGCCCAAC 1541  
 QY 490 SerThrThrValLeuIleGln----- 496  
 Db 1542 TCCCTGCGGTGGGTGAGCGCTTACCTTCAGGGAGAGCTCGTGAGCTCAGAGAGCTTC 1601  
 QY 497 ----- 1601  
 Db 1602 CGTTCACCTATGCAACCTATGAGGCGCTGATAGCGGCTGTGAGCGCTGAGCTGAGCT 1661  
 QY 502 LysGlnValAla----- 505  
 Db 1662 GCTGCTGCTGATGATACAGGCTACCGGAGCTGCGGCGGAGAGCCACTTACTCGTGTGT 1721  
 QY 506 -----ValProAlaThrAsp----- 510  
 Db 1722 GTCATGCTTGTGGGCGCGGCGGCTGCGGAGGAGAGGCTGCGGAGAGGCTCAT 1781  
 QY 511 ThrThrAspLeuMetGlnThrSerLeuAspGluValMetTyrThrTyr 527  
 Db 1782 ACACCCCAGCGCTCACTCAACACAGCCCGGAGTCAAGCCCGGAGGAACTTG 1841  
 QY 528 -----IleIleIleGluCysPheValAlaValThrLeuLeuAlaAlaMetLeuIle 545  
 Db 1842 CCGCTCTCATTTGCGCGCGCGCTGCGCGGCTCTGCGCGGCTGCGGTGCGGTGGG 1901  
 QY 546 ValPheTyrLeuArgTyrGluArgHisGlnArgSerThrValThrAlaAlaArg-- 564  
 Db 1902 GCAAGCTACTGTGTGCGCGG-----GGCGGCGGCACTGAGACAGCGGCTCAGAGAC 1952  
 QY 565 -----ThrValGluIleIleGlnValAsp--- 572  
 Db 1953 AAGAGGAGGTGGGCGCGAGGCTGCGGCTGAGAACTGAGGAGAGAGTCCCTTG 2012  
 QY 573 GluAspIleProAlaIleThrSerAlaAlaAlaThrAlaAlaProSerGluValSerGly 592  
 Db 2013 GAGCCAGCGCCGAGAGCAACAGAGGCGGTGAGAGAGCCCTGCGCGGCTGTGAGTGT 2072  
 QY 593 Glu-----Gly-AlaValValLeuProThrIleHisAspHisIleAsnTyrAs 608  
 Db 2073 GAGGTGCACTGAGGCTTCCAGGAGGCTGAGCTCCAGTCAACCCCTCCAGCAAGAGCC 2132  
 QY 608 nThrTyrLeuProAlaHisGluValAlaIleThrThrGluAsnSerLeuGluYasnSerLeuIle 628  
 Db 2133 TACATCTTAAGCCAGAGAG-----GACAGGCGAGCTGCGGCGGCTC-- 2175  
 QY 628 sProThrValThrThrIleSerGluProTyrIleIleGlnThrHisThrTyrAspTyrVal 648  
 Db 2176 -----TCAGCCAGTGAATGAGCCAGCCCTCTCTGCTGCCACACAGCTAAGTTCTCAGTC 2231  
 QY 648 Igin 649  
 Db 2232 CCAA 2235  
 RESULT 7  
 US-09-063-950-1  
 : Sequence 1, Application US/09063950C  
 : Patent No. 6225085  
 : GENERAL INFORMATION:  
 : APPLICANT: Holzman, Douglas A.  
 : TITLE OF INVENTION: NOVEL LARGE PROTEIN AND NUCLEIC ACID MOLECULES AND USES  
 : FILE REFERENCE: MEI-019  
 : CURRENT APPLICATION NUMBER: US/09/063,950C  
 : NUMBER OF SEQ ID NOS: 9  
 : SOFTWARE: PatentIn Ver. 2.0  
 : SEQ ID NO 1  
 : LENGTH: 2852  
 : TYPE: DNA  
 : ORGANISM: Homo sapiens



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QY 565 -----ThrValGluIleIleGlnValAsp--- 572
Db 1993 AAAGGAGAGTGGGCGAGGGCTGGGCCCCCTGAGACTGGAGGAGGAGTGCCTCCCTG 2052
QY 573 GUAAspIleProAlaIleThrSerAlaAlaIleThrAlaIleProSerGlyValSerGly 592
Db 2053 GAGCGAGCGCCGAGGAGGAGGCGGCTGGAGAGAGCCCTGCGCCAGCGGCTCTGAGTGT 2112
QY 593 Glu-----Gly-AlaValValIleuProThrIleHisAspHisIleAsnTyrAs 608
Db 2113 GAGGTGCACCTCATGGGCTTCCAGGGCTGGCTCCAGTCACTCCCTCCAGCGAAAGCCC 2172
QY 608 nThrTyrIleProAlaHisIleGlyAlaIleStrThrGluAsnSerIleuGlyAsnSerIleuH 628
Db 2173 TACATCTAAGCCAGAGAGA-----GACAGGCGCAGCTGGGCGCGGCTC-- 2215
QY 628 sProThrValThrThrIleSerGluProTyrIleIleGlnThrHisThrIlyAspIlySva 648
Db 2216 ----TCAGCCAGTGAATGCGCAGCCCTCTCTGCTGCCACACAGTAAGTCTCAGTC 2271
QY 648 Iglu 649
Db 2272 CCAA 2275

RESULT 8
US-09-063-950-3
Sequence 3, Application US/09063950C
Patent No. 6225085
GENERAL INFORMATION:
APPLICANT: HOLTZMAN, Douglas A.
TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
FILE REFERENCE: MEI-019
CURRENT APPLICATION NUMBER: US/09/063, 950C
CURRENT FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 2019
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(2019)
US-09-063-950-3

Alignment Scores:
Pred. No.: 4,9e-35 Length: 2019
Score: 416.00 Matches: 180
Percent Similarity: 39.06% Conservative: 93
Best Local Similarity: 25.75% Mismatches: 245
Query Match: 12.07% Indels: 181
Gaps: 26

US-09-991-053-10 (1-653) x US-09-063-950-3 (1-2019)
QY 17 IleIleuProPheValTyrIleuThrAlaGlnValTrpIleuCyAlaIleAla 36
Db 19 CTGCTGCTGCGCTGCTGCTGCTA----- 42
QY 37 AlAlaIleSerAlaGlyProGlnAsnCysProSerValCysSerCysSerAsnGluPhe 56
Db 43 CTGGCCCTGGGGCGCTGGGGCTGCAAGGCTGCCATCCGCTCCAGTGCAGC--CAGCCA 99
QY 57 SerIyValValCysThrArgArgGlyLeuSerGluValProGlnGlyIleProSerAsn 76
Db 100 CAGACAGCTCTTCTCAGCTGCGCCGAGGAGGAGCGAGTGGCCGAGAGTGCACCCGAC 159
QY 77 ThrArgTyrIleuAsnIleuMetGluAsnAsnIleGlnMetIleGlnAlaAspThrPheArg 96
Db 160 ACGGTGGGGCTGTAAGTCTTTGAGAAAGCGATCACTGTCGACGAGCGAGCTTTGCC 219

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QY 97 HisIleuHisIleuGlnValIleuGlnIleuGlyArgAsnSerIleArgGlnIleGluVal 116
Db 220 GGCCTGCCGGGCGCTGCAGCTCTGACCTGTCAAGAACAGATTCGACAGCTGCCAGC 279
QY 117 GlyAlaPheAsnGlyLeuAlaSerIleuSerThrIleuGluIleuPheAsnTrpIleuThr 136
Db 280 GGGGTCTTCAGACCACTCGCCAACTTCAGAACCTGACCTGACGCGCCAGCTGCAT 339
QY 137 ValIleProSer----- 140
Db 340 GAATTCACCAATGAGACTTCCTGCGCTGGCGCTCGAGCGCTCTTACTGGGCAAG 399
QY 141 -----GlyAlaPheGluTyrIleuSerIlySleuArgGluLeu 152
Db 400 AACCGATCCGCCACATCCAGCTGGTGGCTTGACACGCTGCAGCGCTCTCGAGACTC 459
QY 153 TrpIleuArgAsnAsnProIleGluSerIleProSerTyrAlaPheAsnArgValProSer 172
Db 460 AAGCTGAGGAGCAACGAGCTGCGGCGACTGCCCGCTG-----CCCTGCCCGCGC 510
QY 173 LeuMetArgIleuAspIleuGlyGluLeuIlySleuGluTyrIleSerGluGlyAlaPhe 192
Db 511 CTGCTGCTGCTGACCTCAGCCAC--AACAGCTCTCGGCTCGGAGCCGAGCTCTG 567
QY 193 GluGlyLeuPheAsnIleuIlySlyTyrLeuAsnIleuGlyMetCysAsnIleIlyAspMetPro 212
Db 568 GAC---ACTGCCAAGCTGAGAGGCGCTGGCTGGTGTGGGGCTGCAGAGCTGGAC 624
QY 213 Asn-----LeuThrProIleuValGlyLeuGluGluIleuGluMetSerGlyAsnHisPhe 230
Db 625 GAGGGGCTCTTACGCGCTGGCCCAACTCCAGCACTGATGTGTCGCAACAGCTG 684
QY 231 ProGluIleArgProGlySerPheHisGlyLeuSerSerIleuIlySlyLeuTrpAlaMet 250
Db 685 GAGCGAGT---CCACTGTGATCCAGAGCTTCGGGGCGCTGACGCGCTGGCGCTGGC 741
QY 251 ---AsnSerGlnValSerIleuIleGluArgAsnAlaPheAspGlyLeuAlaSerLeuVal 269
Db 742 GCGAACACCGCATTTGCCAGCTGCGGCGCGGAGAGACTGGCCGGCTGGCTGCCCTGCAG 801
QY 270 GluIleuAsnIleuAlaHisAsnAsnIleuSerSerIleuProHisAsp-----LeuPhe 286
Db 802 GACTGTGATGTGACAACTTAAGCTGACAGCCCTGCTGGCAGCACTCGGCGCTCTTC 861
QY 287 ThrProIleuArgTyrIleuValIleuHisIleuHisAsnProTrpAsnCysAspCys 306
Db 862 CCCGCTGCGCTGCTGCGAGCTGCC-----CGCAACCCCTTCAACTGCTGTGC 912
QY 307 AspIleuThrProIleuAlaTrpTrpLeuArgGlu---TyrIleProThrAsnSerThrCys 325
Db 913 CCCTGAGCTGTGTTGGCCCTGGGTGCGGAGAGCACTCACTGGCCAGGCTGGAG 972
QY 326 CysGlyArgCysHisAlaProMetHisMetArgGlyArgTyrIleuValGluValAspGln 345
Db 973 GAGAGCGGTGACACTTCCGCCCAAGAAAGCTGCGGCTGCTCTCGAGCTTGAATAC 1032
QY 346 AlaSerPheGlnCysSerAla-ProPheIleMetAspAlaProArgAspIleuAsnIleSe 365
Db 1033 GCGCACTTGTGCTGCCAGCCACCA-----CCACCAACGCCACAGTGCACC 1080
QY 365 rGluGlyArgMetAlaGluIleuIlySlyArgThrProProMetSerSerValIlyStrPle 385
Db 1081 ACGAGGCCCGTGC-----TCCGGAGGCCCAACAGCTTGTCTTCTTACGCTTGGCT 1128
QY 385 uIleuProAsnGlyThrValIleuSer-HisAlaSerArgHis-----ProArgI 401
Db 1129 CTAAGCTGC-----TTAGCCCAACAGCGCGGCTGAGGCGCCAGCGCGGCC 1179
QY 401 IeSerValIleuAsnArgGlyThrIleuAsnPheSerHisValIleuLeuSerAspThrGly 421
Db 1180 TCACTGCGCCACCGAC----- 1196
QY 421 aTyrThrCysMetGlyThrAsnValAla-GlyAsnSerAsnAlaSerAlaTyrIleuAsn 440

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QY 180 uLeuYslyLeuGluYrIleSerGluGlyAlaPheGluGlyLeuPheAsnLeuYsTy 200
Db 750 A---AAATAGATTGAGATGATCAACAGTAAGTGGTTGATGCTCTTCCAAATCTAGAGAT 806
QY 200 rLeuAsnLeuGly-----MetCyAsnIleYAspMetPro----- 212
Db 807 TCTGATGATGGGAAAATCCAAATTATCAGATCAAAAGACATGAATTTAAGCCTTAT 866
QY 213 -----AsnLeuThr-----ProLe 217
Db 867 CAATCTTGAGAGCTGTTATAGCTGTTATTAACCTCAGAAATACCAATTAACGCTT 926
QY 217 uValGlyLeuGluGlyLeuGlu----- 224
Db 927 GATTGAGCTGAAAACCTTAGAAGCATCTCTTTAGATTAACGCTTATTAAGTACC 986
QY 225 -----MetSerGlyAsnHisph 230
Db 987 CCATGTTGCTCTTCAAAAAGTTGTAATCTCAAAATTTTGGATCTAATAAATCCTAT 1046
QY 230 eProGluIleArgProGlySerPheHisGlyLeuSerSerLeuYslyLeuTyrVal-- 249
Db 1047 TAATAGAAATACGAAAGGGGTATTTAGCAATATGCTACACTTAAGAGATTGGGATAAA 1106
QY 249 ----- 249
Db 1107 TAATATGCTGAGCTGATTTCCATCATGATGCTGCTGTGATTAACCTGCCAAGTTTAAG 1166
QY 250 -----MetAsnSerGlnValSerLeuIleGluYrAsnAlaPheAspG1 264
Db 1167 AAAAATAGAAAGCTACTAACAACCTTAATGTTGTTTACATTCACCCCAATGATTTTTCAG 1226
QY 264 yLeuAlaSerLeuValGluLeuAsnLeuAlaHisAsnAsnLeuSerSerLeuProHisAs 284
Db 1227 ACTCCCAAGCTGGAATCAGTCACTGTAACAGCAAGAACTCTGCTGATCCCTGTAACATGG 1286
QY 284 pLeuPheThrProLeuArgYrLeuValGluLeuHisIleuHisIleAsnProTyrAsnCy 304
Db 1287 TACCATGAGATCTCTGCCAAACCTCAAGGAATACAGCATACAGTAAACCCATCAGATG 1346
QY 304 sAspCyAspIleLeuTyrLeu-----AlaTyrIleuYrGluYrIleProth 321
Db 1347 TGACTGTGTCATCGTTGATGATGACATGAACAAACCAATTCGATTCATGAGCCAGA 1406
QY 321 rAsnSerThrCySerGlyArgCyHisIlePheMetHisMetArgGlyArgYrLeuVal 341
Db 1407 TTCACGTGTTTGCCTGAGC-----CCACCTGAATTCCAAGTCCAGAAATGTTGC 1454
QY 341 lGluValAsp---GlnAlaSerPheGlnCySerAlaProPheIleMet-----AspAl 358
Db 1455 GCAAGTGCATTTCCAGGACATGATGAAATTTGCTCCCTTTATAGCTCTTGAGACTT 1514
QY 358 aProArgAspLeuAsnIleSerGluGlyArgMetAlaGluLeuYsCyArg-----Th 376
Db 1515 TCCCTTAATCTAATATGAGAGCTGGAGCTATGTTCTTCCACGTAGAGTACTGCC 1574
QY 376 rProPheMetSerSerValIlyTyrPheLeuProAsnGlyThrValLeuSerHisAlaSe 396
Db 1575 AGAACCAACAGCTGAATCTAAGTAAACACCTTCTGTCMAAACTCTTGCCCTTAATAC 1634
QY 396 rArgHisProArgIleSerValIleuAsnAspGlyThrLeuAsnPheSerHisValLeuLe 416
Db 1635 CTGACAGACAAAGTTCTATGCTCATTTCTGAGGAAACCTAGATTAATAGCGCTTAAC 1694
QY 416 uSerAspThrGlyValIlyThrCySerGlyThrAsnValAlaGlyAsnSerAsnAlaSe 436
Db 1695 CAAAGAAAGGGGTTTATATCTGTATAGCAATCACTAGTGGCGGTGACTTGAAGTCC 1754
QY 436 rAlaTyrLeu-----AsnGlySerThrAlaGluLeuAsnThrSerAsnYrSerPheph 454
Db 1755 TGTATGATCAAAAGTATGATGATCTTTTCCACAGATTAACAATGCTCTTTGAATATT-- 1812

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QY 454 ethrThnglyThrGlyGluThrThrGluIleSerProGluAspThrThrArgYsTy 474
Db 1813 -----AAATAGAGATATTACAGGCCAATTCACTTGGTGTCCGGA 1856
QY 474 s-----ProValProThrThrSerThrGlyYrGlnProAlaTyrThrThrSerTh 491
Db 1857 AGCAAGTTCTAAATCTCAAACTAGTGTAAATGACAGCCCTTGTCAAGACTGAAA 1916
QY 491 rThrValLeuIleGlnThrThrArgValProYsGlnAlaVal----- 506
Db 1917 TTTCATGCTGCGCAAGTCTCGAATACCATGATGATCAAGGTATATATCTACTCA 1976
QY 507 -----ProAlaThrAsp 510
Db 1977 TGTGAATCCATCAACTGAG 1995

RESULT 10
US-09-188-930-228
/ Sequence 228, Application US/09188930A
/ Patent No. 6150502
/ GENERAL INFORMATION:
/ APPLICANT: Watson, James D.
/ APPLICANT: Strachan, Lorna
/ APPLICANT: Sleeman, Matthew
/ APPLICANT: Onrust, Rene
/ APPLICANT: Murison, James Greg
/ TITLE OF INVENTION: Compositions Isolated From Skin Cells
/ TITLE OF INVENTION: and Methods For Their Use
/ FILE REFERENCE: 11000.1011c1
/ CURRENT APPLICATION NUMBER: US/09/188,930A
/ CURRENT FILING DATE: 1998-11-09
/ NUMBER OF SEQ ID NOS: 348
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 228
/ LENGTH: 2296
/ TYPE: DNA
/ ORGANISM: Mouse
/ FEATURE:
/ NAME/KEY: ununre
/ LOCATION: (2255)...(2255)
US-09-188-930-228

Alignment Scores:
Pred. No.: 1,84e-33 Length: 2296
Score: 402.50 Matches: 169
Percent Similarity: 39.00% Conservative: 95
Best Local Similarity: 24.96% Mismatches: 259
Query Match: 11.68% Indels: 155
DB: Gaps: 23

US-09-991-053-10 (1-653) x US-09-188-930-228 (1-2296)
QY 37 AlAlaAlaSerAlaGlyProGlnAsnCyAspSerValCySerYAsnGlnPhe 56
Db 248 GCACTGTGTCAGTGTGGCTAAATCTGTCATCTGTATGCTGTGACGAGCTTC 307
QY 57 SerIyValValCyThrIArgArgGlyLeuSerGluValProGlnGlyIleProSerAsn 76
Db 308 -----ATTACGTAAAGATCGCTCTGACATTCACATTCAGTGGAAATTCGAGAGAT 361
QY 76 ----- 76
Db 362 GCTAACAACTCTTACCTTCAGAACCAACCAATAAACAATGTGGGATTCCTCCGATTGG 421
QY 76 ----- 76
Db 422 AGAACTTGCTGAAGTAAAGATATACCTATACCAACAAGTTTATGATGATTCCT 481
QY 77 -----ThrArgYrLeuAsnLeuMetGluAsnIleGlnMetIle 90
Db 482 ACCAACCTTCCAAAGTATGTCAAAGAGTTCATTTGCAAGAGATTAACATAGAGACTATC 541
QY 91 GlnAlaAspThrPheArgHisIleuHisIleuGluValLeuGluIleuGlyArgAsnSer 110

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Db 542 ACCTATGATCACTTCGAAATTCGATCTCGAAGAGTTACACTTGATGATTAACCA 601
Qy 111 ILeArg-----GInIIeGIuValGIyValAheAnGIyLeuAlaSerLeuSerThreU 128
Db 602 GTCGCGCTGTAGCATGAAGAGGACATTTCCAGACAGTAACATATCTCGCGCTGCTT 661
Qy 129 GlUeuPheAsePentPLeuThrValIIeProSerGIyAlaPheGIUyLeuSerLys 148
Db 662 TTTCTGTCCGTAACCACTTAGCAACATCCCGGGGGCTTCCAGAGACATATTAGAA 721
Qy 149 LeuIleGIUeuThrPLeuArgAseAnbProIIeGIUeuSerIIeProSerTyAlaPheAn 168
Db 722 TTACGC-----CTGATGACCAATCGCATATCAACGATCTTCCCATCACTTCAT 772
Qy 169 ArgValProSerLeuMetArgLeuAsePLeu---GIyGIUeuLysLysLeuGIUyTrIle 187
Db 773 GGTCTCACAGCGCTGAACCGCTGGTTTATAGTGAACCTGTGTGAACACCATGGTTTG 832
Qy 188 SerGIUyAlaPheGIUyLeuPheAnLeuLysTyTrLeuAnLeuGIyMetCyAseAn 207
Db 833 GGTGACAAAGTTTCTTCACTTACTTAACATTAACAGACCTGTCTCTGTGAGGAATTC 892
Qy 208 ILeuAsePMetPro---AseLeuThrProLeuValGIyLeuGIUyLeuGIUeMetSer 226
Db 893 TTGACAGACGCGCCAGTAACCTT----- 916
Qy 227 GlyAseNHisPheProGIUyIleArgProGIySerPheNIIeGIyLeuSerSerLeuLys 246
Db 917 -----CCGCGC-----ACAGCCTGAGAG 937
Qy 247 LeuTrpValMetAseSerGIUyValSerLeuIleGIUyAseAnIaPheAseGIyLeuAla 266
Db 938 CTTTACCTTCAAGAACATATCAACCGGGATCCCAATGCTTTTCTTATTATAGG 997
Qy 267 SerLeuValGIUyLeuAnLeuAlaHisAseAnLeuSerSerLeuProHisAsePLeu 286
Db 998 CAGCGTATCGATCGATATGCTTAATATTAACATTAACATTAACATTAACATTAAC 1057
Qy 287 ThrProLeuArgTyTrLeuValGIUeuNHisAseAnProTrpAseNHisAsePLeu 306
Db 1058 GATGATTTGACAAATATTAACCACTGATTTCTTCCAAACATTCCTTGGTATTGTGAAGC 1117
Qy 307 AsePLeuLeuTrpLeuAlaTrpTrpLeuArgGIUyTrIleProThraAseNHisAsePLeu 326
Db 1118 AAGATGAATGGGTAACGAGCTGTACATCG---CTACCGGTGAAGTCAATGTGCT 1174
Qy 327 GIY---ArgCyAseNHisAsePLeuMetAsePLeuArgTyTrLeuValGIUyAsePLeu 345
Db 1175 GGGCTCATGTCCCAAGCCCAAGAAAGGTCCGTGAATGGCTATCAAGACCTCATGTCA 1234
Qy 346 AlaSerPheGIUySerSerAlaProPheIIeMetAsePLeu----- 358
Db 1235 GAACGTGTTGATTTGAAGACAGTGGATTTGAGACCACTTACATTAACCACTGCAATA 1294
Qy 359 ProArgAsePLeuAseNIIeSerGIUyArgMetAlaGIUeuLysCyAseNHisAsePLeu 378
Db 1295 CCCAACAAGACATATCTCTCAAGACAGTGGCCAGCTCTCTGTGACCAAAACAACAT 1354
Qy 379 MetSerSerValIyTrpLeuProAnGIyThraValLeuSerHisAsePLeuHis 398
Db 1355 ATTAAACCCCAAG---CTCATTTAAGGATCAGCAATACAGGACGCCCTCAGGAAA 1411
Qy 399 ProArgIIeSerValLeuAsePLeuArgTyTrLeuAseNHisAsePLeuValLeuSerAseP 418
Db 1412 ACAATTTTAATTAAGTGAATCTGTCAACCCCTCAACATTCACATATTC-CTGAGACT 1470
Qy 419 ThrGIyValTyTrHISyMetGIyThraAseNValaGIyAseN-SerAseNIIeSerAlaTy 438
Db 1471 TGCTCTGCTTATGACTGTGCACTCAGCTGGCTTTAACTGGGCCATTAAGCCACCTT 1530
Qy 438 rLeuAseNIIeSerThraIaGIUyLeuAseNHisAsePLeuSerPheNHisAsePLeuThra 458

```

```

Db 1531 T-----GATCTATTAACAGAA-----ACAACTGTAAAC 1557
Qy 458 rGIyGIUyThrArgIu-----IIeSerProGIUyAsePLeuThraArgTy 473
Db 1558 AGGAAACGCACTAATTAATCTGTGACCGCCCTTAAGAACCTTAATCAACCTTAATGATG 1617
Qy 473 rLyAsePLeuAProThrThraSerThraGIyTrGIUyProAlaTyThrThraSerThraVa 493
Db 1618 CATGTTTCCCAATGAACCAAGTAACTTTAC-----CTGTTTATGAACAACCTGT 1668
Qy 493 IIeNIIeGIUyThraThraArgValProLyGIUyAlaValaProAlaThraPLeuThra 513
Db 1669 TTGATTGAGACCCCAACCTGCTTCAATGTACAAACCCCAACCC---ACCTTCA 1725
Qy 513 pLyMetGIUyThraSerLeuAsePLeuValMetLyThrThraLysIle-----II 529
Db 1726 TCGAGAGCAAGAGAA-----GAACCTTACAAATTCAAATTTACTTGGCTGCCAT 1779
Qy 529 eIIeGIyCyAsePLeuAlaValaThraLeuAlaAlaMetLeuIleValPheTy-- 548
Db 1780 CATTGGTGGGCTGTGGCCCTGTGAACATGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 1839
Qy 549 -----LysLeuArgLyAsePLeu 554
Db 1840 GCATAGAACCGGTCACTGTTTTCACGGAACCTGCGTACAGAAAGCGGAGAGAGAA 1899
Qy 554 eGIUyGIUySerThraThraIaAlaArgThraValGIUyIleGIUyValaAsePLeu 574
Db 1900 GGATGACTATGCAACACCGGTACTTAAGAAAGACAACTCCATCTTGAAGAACAGAGAAC 1959
Qy 574 p-----IIeProAlaIaThraSerAlaAlaIaThraIaAlaProSerGIyVa 590
Db 1960 TTTCTTCCAGATGCTACG-----AT 1980
Qy 590 ISeGIyGIUyAlaValaValaLeuProThraIleHisAsePLeuIleAseNHisAsePLeu 610
Db 1981 AAGCAAGAA-----CCCATCTCCAGAGAGAGTGTGAATACACACCAT 2025
Qy 610 rLyProAlaHisGIyAlaHisTrpThraIaAsePLeuGIUyAsePLeu 626
Db 2026 ATTTCTTCCGATGATGAATCTGTACAAAGAACCACTCATGAGAGC 2074

RESULT 11
US-09-312-283C-228
; Sequence 228, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Orntus, Rene
; APPLICANT: Muriison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; FILE REFERENCE: 11000.1011C2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 228
; LENGTH: 2296
; TYPE: DNA
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2296)
; OTHER INFORMATION: n = A,T,C or G
US-09-312-283C-228

Alignment Scores:
Pred. No.: 1,84e-33 Length: 2296
Score: 402.50 Matches: 169

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Percent Similarity: 39.00%  
 Best Local Similarity: 24.96%  
 Query Match: 11.68%  
 DB: 4  
 Gaps: 23

US-09-991-053-10 (1-653) x US-09-312-283C-228 (1-2296)

Conservative: 95  
 Mismatches: 259  
 Indels: 155

37 AlaAlaIaSerAlaGlyProGlnAsnCyseProSerValCyseSerCyseSerAlaGlnPhe 56  
 248 GCACCTCTGTCAGTGGTAAATCCGTGCATCTGATGTGCTGACGACGAGCTTC 307  
 57 SerIysValValCysThrArgArgGlyLeuSerGluValProGlnGlyIleProSerAsn 76  
 308 ---ATTACTGTAAAGCATGCTCTGTACATCCATTCACAGTGGGAATCCGAGAGAT 361  
 76 ---  
 362 GCTAAACAACCTTACCTTCAGAACACCAATTAACAATGTTGGGATTCCTTCGATTTG 421  
 76 ---  
 422 AAGAACTTGTCTGAAGAAGTAAAGAAATATACCTATACCAACAACAGTTAGATGATTCCT 481  
 77 ---  
 482 ACCAACCCTTCCAAAGTATGTCAAGAAGTTACATTTGCAAGAAATACATAGAGACTATC 541  
 91 GlnAlaSerThrPheArgHisIleuHisIleuGluValLeuGlnLeuGlyArgAsnSer 110  
 542 ACCTATATATCACTTGGAAATATCCGTATGTGAAGAAGTTACCTGGATGATTAACCTCA 601  
 111 IleArg-----GlnIleGluValGlyAlaPheAsnGlyLeuAlaSerIleuSerThrIleu 128  
 602 GTCGCGCTGTATACATCGAAGAGGAGCATTTGAGACATATCTACCTGCGCTGT 661  
 129 GluLeuPheAsnThrPleuThrValIleProSerGlyAlaPheGlyIleuSerIys 148  
 662 TTTCTGCCCTGATCAACCTTACGACAAATCCGGGGGCTTCCGACGATTAAGAGAA 721  
 149 LeuArgGluLeuThrPleuArgAsnAsnProIleGluSerIleProSerThrAlaPheAsn 168  
 722 TTACGC-----CTGGATGACATCGATCAATCAAGATCTTCCCATCACTTCCAT 772  
 169 ArgValProSerLeuMetArgLeuAspLeu---GlyGluLeuGlyIleGluGlyIle 187  
 773 GGTCTCACAGCCTGAAACGCTGTTTACATGGAACCTTGTGACACACAGGCTTTC 832  
 188 SerGlnGlyAlaPheGlnGlyLeuPheAsnLeuIysThrLeuAsnLeuGlyMetCysAsn 207  
 833 GGTGACAAAGTTTCTTCACTAGTAACTTAACAGAGCTGTCCCTGTGAGGAAATTC 892  
 208 IleIysAspMetPro---AsnLeuThrProLeuValGlyLeuGluGluLeuMetSer 226  
 893 GTTGACAGCAGCGCAAGTGAACCTT-----  
 227 GlyAsnHisPheProGluIleArgProGlySerPheHisGlyLeuSerSerLeuIys 246  
 917 ---  
 247 LeuThrValMetAsnSerGlnValSerLeuIleGluArgAsnAlaPheAspGlyLeuAla 266  
 938 CTTTACCTTCAAGACACATATCAACCGGGTACCCCAATGCTTTTCTTATTTAAG 997  
 267 SerLeuValGluLeuAsnLeuAlaHisAsnAsnLeuSerSerLeuProHisAspLeuPhe 286  
 998 CAGTGATTCAGCATGTATGTATATTAATTAACCTTAACCAATTTACCTCAGGGTATCTTT 1057  
 287 ThrProLeuArgGlyLeuValGluLeuHisIleuHisIleuProThrAsnProCysAspCys 306  
 1058 GATGATTTGACATATATCAACCACTGATTTCTTCCAAACATCTTGGTATTTGGATGC 1117  
 307 AspIleLeuThrPleuAlaThrPleuArgGlyIleProThrAsnSerThrCysCys 326

1118 AAGATGAATGGGTACAGACTGGTTACAGTGC---CTACCGGTGAAGGTCAATGTGCGT 1174  
 327 Gly---ArgCysHisAlaProMetHisMetArgGlyArgGlyLeuValGluValAspGln 345  
 1175 GGGCTCATGTGCCAAGCCCAAGGAAAGGTCCGTGGATGGCTATCAAGACCTCAGTCA 1234  
 346 AlaSerPheGlnCysSerAlaProPheIleMetAspAla----- 358  
 1235 GAACGTGTTGATGTATAAGACAGTGGATTTGTGACACCATTCAGATTAACCATGACATA 1294  
 359 ProArgAspLeuAsnIleSerGlnGlyArgMetAlaGluLeuIysCysArgThrProPro 378  
 1295 CCCAACAACAGATATCTGTGTCAAGACAGTGGCCAGCTCTGTGACCAACAACAGAT 1354  
 379 MetSerSerValIysThrPleuProAsnGlyThrValLeuSerHisAlaSerArgHis 398  
 1355 ATTAAAAACCCAG---CTCATTAAGATTCAGGAATCTACAGGACCCCTCAGGAA 1411  
 399 ProArgIleSerValIleuAsnAspGlyThrIleuAsnPheSerHisValLeuLeuSerAsp 418  
 1412 ACAATTTTATTACTGTGAATGTGTCAACCCCTGACACATCCACATATC-CTGGAGACT 1470  
 419 ThrGlyValIysThrCysMetGlyThrAsnValAlaGlyAsn-SerAsnAlaSerAlaTy 438  
 1471 TGCTGTCTATGACTCTGTGACACTCAGCTGCTTAACCTGGCCATAGCCAGCCTT 1530  
 438 rIleuAsnGlySerThrAlaGluLeuAsnThrSerAsnItySerPheThrThrGlyTh 458  
 1531 T-----GAGTCTTAACAGAA-----ACAAATCGTAAC 1557  
 458 rGlyIleuThrThrGlu-----IleSerProGluAspThrThrArgIysTy 473  
 1558 AAGGAAGACGAGTAAATCTGTGCACCGCCCTGAACCTGAATACCCCTATAGATAG 1617  
 473 rIysProValProThrThrSerThrGlyTyGlnProAlaTyThrThrSerThrIysVa 493  
 1618 CATGGTTCCTAGTGAACCAAGTAACTTTAC-----CTGTGTGATGAACACCTGT 1668  
 493 IleuIleGlnThrThrArgValProIysGlnValAlaValProAlaThrAspThrThrAs 513  
 1669 TTGATTTGACGCCAAGCTGCCCTTTCGAATGTACAAACCCCAACCC--ACCTTCAA 1725  
 513 rIysMetGlnThrSerLeuAspGluValMetIysThrThrIysIle-----11 529  
 1726 TCGAGACCAAGAA-----GAACCTTACAAAATCCAAATTACTCTTGCGTGCAT 1779  
 529 eIleGlyCysPheValAlaValThrLeuLeuAlaAlaMetLeuIleValPheTy-- 548  
 1780 CATGTGTGGGCTGTGGCCCTGTAAACATCGCCCTCTTGGTGTGTGTATGT 1839  
 549 -----LysLeuArgIysArgHis 554  
 1840 GCATAGAACCGGTCACTGTTTTCACGGAACGTGCTGACAGAAAGCGGAGAGAA 1899  
 554 sGlnGlnArgSerThrValThrAlaAlaArgThrValGluIleGlnValAspGluAs 574  
 1900 GGATGACTATGCAGAACCGGTACTAAGAAAGACAACTCCATCTTGAAATCAGGAAAC 1959  
 574 P-----IleProAlaAlaThrSerAlaAlaAlaThrAlaAlaProSerGlyVa 590  
 1960 TTTCTTCCAGATGCTACG-----AT 1980  
 590 IserGlyGluGlyAlaValAlaValLeuProThrIleHisAspHisIleAsnTyIAsnThrTy 610  
 1981 AAGCAATGA-----CCCATCTCCAAAGAGAGATTGTGAATACACACAT 2025  
 610 rIysProAlaHisGlyAlaHisIleThrGlnAsnSerLeuGlyIleAsnSer 626  
 2026 ATTTCCTCCGAATGAGATGATCTGTACAAAGAACACTCAGTAGAGC 2074

RESULT 12  
 US-09-484-970B-66  
 / Sequence 66, Application US/09484970B

Patent No. 6426186  
 GENERAL INFORMATION:  
 APPLICANT: Jones, Karen A.  
 APPLICANT: Volkovich, Wayne  
 APPLICANT: Walker, Michael G.  
 TITLE OF INVENTION: BONE REMODELING GENES  
 FILE REFERENCE: PB-0014 US  
 CURRENT APPLICATION NUMBER: US/09/484,970B  
 CURRENT FILING DATE: 2000-01-18  
 NUMBER OF SEQ ID NOS: 172  
 SOFTWARE: PERL Program  
 SEQ ID NO 66  
 LENGTH: 6814  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc feature  
 OTHER INFORMATION: Incyte ID No. 6426186 199882.3  
 NAME/KEY: unsure  
 LOCATION: 1838, 5528  
 OTHER INFORMATION: a, t, c, g, or other  
 US-09-484-970B-66

Alignment Scores:  
 Pred. No.: 2,37e-32 Length: 6814  
 Score: 400.00 Matches: 160  
 Percent Similarity: 33.94% Conservative: 81  
 Best Local Similarity: 22.54% Mismatches: 239  
 Query Match: 11.61% Indels: 230  
 Gaps: 20

US-09-991-053-10 (1-653) x US-09-484-970B-66 (1-6814)

Qy 18 LeuLeuProPheValTyrLeuThrAlaGlnValTrrPleLeuCyAlaAlaIleAla 37  
 Db 91 CTGTGGCGCTGCTGCTCTTCTGCGCC-----TGGGGAGCGCTGGCGGTGGCCAG 144  
 Qy 38 AlaAlaSerAlaGlyProGlnAsnCySerProSerValCySerCySerAsnGlnPheSer 57  
 Db 145 AAGCGCGCGCGAGG-----TGTCGAGCCCGCTCCCTGCTTCCG-----ACC 189  
 Qy 58 LysValValCysThrArgArgGlyLeuSerGluValProGlnGlyLeuProSerAsnThr 77  
 Db 190 ACCGGCGCTGCATCTCTGCTGAGGCGCGCGCGCGCGCGCGCGCGCGAGACTCC 249  
 Qy 78 ArgTyrLeuAsnLeuMetGluAsnAsnIleGlnMetIleGlnAlaAspThrPheArgHis 97  
 Db 249 ----- 249  
 Qy 98 LeuHisIleLeuGluValLeuGlnLeuGlyArgAsnSerIleArgGlnIleGluValGly 117  
 Db 250 -----ATCTAGATCTTCTGCTTAAACAGATCAAGAGATCAACACTGGG 294  
 Qy 118 AlaPheAsnGlyLeuAlaSerLeuSerThrLeuGlnLeuPheAsnTrpLeuThrVal 137  
 Db 295 GCATTCAGCGCGCTGAGGAACCTTGAACACTTCTTCATTAATTAATCAATCAAGAG 354  
 Qy 138 IleProSerGlyAlaPheGlnTyrLeuSerLysLeuArgGluLeuTrpLeuArgAsn 157  
 Db 355 ATACTACTGTGAGCACTTGAAGAACTTGAATAATCTTACTATCTTACAGAGAT 414  
 Qy 158 ProIleGlnSerIleProSerTyrAlaPheAsnArgValProSerLeuMetArgLeuAsp 177  
 Db 415 GAGATCCAGTCAATTGACAGGACGACATTAAAG----- 447  
 Qy 178 LeuGlyGluLeuLysLeuGlnTyrIleSerGlnGlyAlaPheGlnGlyLeuPheAsn 197  
 Db 447 ----- 447  
 Qy 198 LeuLysTyrLeuAsnLeuGlyMetCysAsnIleLysAspMetProAsnLeuThrProLeu 217  
 Db 447 ----- 447

Qy 218 ValGlyLeuGlnGluLeuGlnMetSerGlyAsnHisPheProGlnIleArgProGlySer 237  
 Db 447 ----- 447  
 Qy 238 PheHisGlyLeuSerSerLeuLysLeuLeuTrpValMetAsnSerGlnValSerLeuIle 257  
 Db 448 -----GCACTGGCTCTTCAAGCAACTTACCTGACCTTAAATCAAGATGAAGAACTTTG 501  
 Qy 258 GluArgAsnAlaPheAsnGlyLeuAlaSerLeuValGluLeuAsnLeuAlaHisAsn 277  
 Db 502 GACCAAGATTCGTTCCAGCATCTCCGAGCTCGAAGGCTAATTTTGCATTAACACCGG 561  
 Qy 278 LeuSerSerLeuProHisAspLeuPheThrProLeuArgTyrLeuValGluLeuHisLeu 297  
 Db 562 ATTAACATTTAGTCCAGGAGCATTTAATCACTTGAATCTGAATGAAGAGATTCGACTG 621  
 Qy 298 HisHisAsnProTrpAsnCyAspCyAspIleLeuTrpLeuAlaTrpTrpLeuArgGlu 317  
 Db 622 GACTCAACACACTTCACTGCACTGCACTGCAATCTGTGGTGGCGGATTTGCTGAACCC 681  
 Qy 318 TyrIleProThr-----AsnSerThrCysCysGlyArgCysHisAlaProMetHisMetArg 336  
 Db 682 TACCGGAGTGGGGAAGCGCGCAGCGAGCGGCACTGTGAATATCCAGAGCGCATCGAG 741  
 Qy 337 GlyArgTyrLeuValGluValAspGlnAlaSerPheGlnCysSerAlaProPheIleMet 356  
 Db 742 GAGCGCTCAGTGGGAGCAACATCACCCCGGAGAGCTGAAGCTGAAGAGCCCGGATCAC 801  
 Qy 357 AspAlaProArgAspLeuAsnIleSerGlnGlyArgMetAlaGluLeuLysCyValArgThr 376  
 Db 802 TCCGAGCCCGAGGAGCGAGATGTGACTCTCGGGGAACCCGTACTTCACTGCGAGAGCC 861  
 Qy 377 Pro-----PrometSerSerValTyrTrpLeuLeuProAsnGlyThrValLeuSerHis 394  
 Db 862 GAAGGCAACCCCAAGCTGAGATATCTGGTGAAGAAACAATATGAGCTG-----AGC 915  
 Qy 395 AlaSerArgHisProArgIleSerValLeuAsnAspGlyThrLeuAsnPheSerHisVal 414  
 Db 916 ATGAAGACAGATTCGCCCTTAATCTGTGAGCATGGAGCCCTGATGATCCAGAACCA 975  
 Qy 415 LeuLeuSerAspThrGlyValTyrThrCysMetGlyThrAsnValAlaGlyAsnSerAsn 434  
 Db 976 CAGGAGACAGACCGAGGATATACAGTGCATGCAAGCAAGACGTGGCGGGA----- 1026  
 Qy 435 AlaSerAlaTyrLeuAsnGlySerThrAlaGluLeuAsnThrPheSerAsnTyrSer----- 452  
 Db 1027 -----GAGGTGAAGACGCAAGAGTGACCTCAGG 1056  
 Qy 453 PhePheThrThrGlyThrGlyGluThrThrGluIleSerProGluAspThr----- 469  
 Db 1057 TACTTCGGGTCTCCAGCTCCAGCCCACTTTGTATCCAGCCAGCAAGATACAGAGTGTCTG 1116  
 Qy 470 ThrArgLysTyrLysProValProThrThrSerThrGlyTyrGlnProAlaTyrThrThr 489  
 Db 1117 GTTGGGAGAGCGTCAGCTGAGTGCAGCGCCACAGCGCACCCCGCGCGGATCTCC 1176  
 Qy 490 SerThrThrValLeuIleGlnThrThrArgValProLysGlnValAlaValProAlaThr 509  
 Db 1177 TGGAGC-----AAGGTGACCGCACACCTTGCCAGTTGAC-----CCGCGGGGTG 1221  
 Qy 510 AspThrThrAsp----- 513  
 Db 1222 AACATCACGCTTGTGGCGGCTTACATACAGAACGTCGACAGGGGAGACGGGAGAG 1281  
 Qy 514 -----LysMetGlnThrSerLeuAspGluValMetLysThrThrLysIleIle 530  
 Db 1282 TATCGGTGCTCTGGACCAACACATGACGCTCCATGCGACCGCTTTCATCATGCTC 1341  
 Qy 531 GlyCysPheValAlaValThrLeuLeuAlaAlaMetLeuIleValPheTyrLysLeu 550  
 Db 1342 CAGGCTCTTCTCAGTTCACGTGAGC----- 1368  
 Qy 551 ArgLysArgHisGlnGlnArgSerThrValThrAlaAlaArgThrValGluIle----- 568



Db 1369 -----CCTCAGACAGAGTGGTTATTGAGGCCAAGACCCTGATTCACGT 1416  
||| ||| ||| :||| ||| :|||  
Qy 569 -----IleGlnValAsp 572  
||| ||| ||| :|||  
Db 1417 GAA GCCCAAGGCAACCCGCCCGCTCATCGCTTGACCAAGAGAGGAGGCACACTTCC 1476  
||| ||| ||| :|||  
Qy 573 GluAspLeuProAlaIaIaThrSerAlaAlaIaIaThrAlaIaIaProSerGlyValSerGly 592  
:||||| :||| :||| :||| :|||  
Db 1477 GTGAACCGCGCGCACCTGGTCTCTCAACCGGAAACCTTAGAATCTCTGGGTTGGCC--- 1533  
:||||| :||| :||| :||| :|||  
Qy 593 GluGlyAlaValValLeuProThrTrtIleHisAspHisIleAsnTYrAsnThrTyLysPro 612  
:||||| :||| ||| ||| |||  
Db 1534 -----CTCCACGACCAAGGCCAGTACGAATGCCAG-- 1563  
:||||| :||| ||| ||| |||  
Qy 613 AlaHisGlyAlaHisTrpThrGluAsnSerLeuGlyAsn----- 625  
:||||| :||| ||| ||| |||  
Db 1564 -----GCTGTCAACATCATCGCTCCCAAGAAGTGTGGCCCACTG 1605  
:||||| :||| ||| ||| |||  
Qy 626 SerLeuHisPProThrValThrThrIle----- 634  
:||||| :||| ||| ||| |||  
Db 1606 ACTGTGCAGCCCAAGTGCATCCCCAGTGTTCGCCAGCATTTCCACAGACAACAAGTGGAG 1665  
:||||| :||| ||| ||| |||  
Qy 635 -----SerGluProTYrIleIleGlnThr 642  
:||||| :||| ||| ||| |||  
Db 1666 GTGGCGCCCAATGTGCAGTCCCCTGTGCACTCCCAAGGCGAGCCGAGCCAGCATTCACC 1729  
:||||| :||| ||| ||| |||  
Qy 643 HisThrLysAspLysValGlnGluThrGln 652  
:||||| :||| ||| ||| |||  
Db 1726 TGGAAACAAGATGGGGTTCAAGTGCACAGAA 1755

RESULT 13  
 US-09-131-648-4  
 Sequence 4, Application US/09131648  
 Patent No. 6168920  
 GENERAL INFORMATION:  
 APPLICANT: Hillman, Jennifer L.  
 APPLICANT: Yue, Henry  
 APPLICANT: Corley, Neil C.  
 APPLICANT: Guegler, Karl J.  
 TITLE OF INVENTION: EXTRACELLULAR ADHESIVE PROTEINS  
 FILE REFERENCE: PP-0576 US  
 CURRENT APPLICATION NUMBER: US/09/131,648  
 CURRENT FILING DATE: 1998-08-10  
 NUMBER OF SEQ ID NOS: 5  
 SOFTWARE: PERL Program  
 SEQ ID NO 4  
 LENGTH: 2290  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE: -  
 OTHER INFORMATION: 2687731  
 US-09-131-648-4

Alignment Scores:	
Pred. No.:	3..9e-33
Score:	399.50
Percent Similarity:	40.14%
Best Local Similarity:	25.33%
Query Match:	11.59%
DB:	3
	Gaps:
	17

OY	74	ProserSerhThraGlyrLysLeuAsnLeuMetGlnAsnAsnIleGlnMetIleGlnAlaAsp	93
DB	264	CGAGCTTACACACAGATTCTTCTCTACAGCTACACATTCGAAAAATTGAACTACC	323
OY	94	ThrPheArgHisLeuHisIleLeuGluValLeuGlnLeuGlyArgAsnSerIleArgGln	113
DB	324	ACGAGCTTCCAGTA---AACCTTACCTGGCTGGATTATCTCAAAAACATTATCTTCA	380
OY	114	IleGluValGlyAlaPheAsnGlyLeuAlaSerLeuSerThrIleGluLeuPheAspAsn	133
DB	381	GTCAACCAATATTATATGTAATAAAAAAGATGCTCAGCTCTCTTCTGTGATCTGAGAGAAAC	440
OY	134	TryPheThrValIleProSerGlyAlaPheGluTyrIleSerLysLeuArgGlnLeuTrp	153
DB	441	AAACTTTCAGTACGCTGAAAAAATGCTGTCTCCAGCTGAGCAACTTACCAAGAACTCTAT	500
OY	154	LeuArgAsnAsnProIleGluSerIleProSerTyrAlaPheAsnArgValProSerLeu	173
DB	501	ATTATATACAACTTGCTTTCTACAAATTTCACTGGAGCTTTATTTGGCTTACATATCTT	560
OY	174	MetArgLeuAsnLeuGlyGluLeuValysLeuGluTyrIleSerGluGlyAlaPheGlu	193
DB	561	CTTGACCTCATCTCAATCA---AATAGATTGCAGATGATCAACAGTAAGTGGTTGAT	617
OY	194	GlyLeuPheAsnLeuLysTyrLeuAsnLeuGly-----MetCysAsnIleLysAsp	210
DB	618	GCTTCTTCCAAATCTAGAGATTCTGATGATTGGGAAAAATCCAAATTATCAGAAATCAAGAC	677
OY	211	MetPro-----AsnLeuThr	215
DB	678	ATGAACTTTAAGCTCTTATCAATCTTCGCGAGCTGGTTATAGCTGGTATTAACCTCACA	737
OY	216	-----ProLeuValGlyLeuGluGluLeuGlu-----	224
DB	738	GAATATACAGATAACGCTTGTTGGATGGAATGGAATAAATAGAACATCTTTTAAAGAT	797
OY	224	-----	224
DB	798	AACAGCTTATTAAGTACCACCATGTTGCTCTTCAAAAAGTTGTAAATCTCAAAATTTTGG	857
OY	225	---MetSerGlyAsnHisPheProGluIleArgProGlySerPheHisGlyLeuSerSer	243
DB	858	GATCTAAATTAATAATTCCTATTATTAAGATATAGAAAGGGGTGATTTTACGATATGCTACAC	917
OY	244	LeuLysLysLeuVal-----	249
DB	918	TTAAAGAAGTTGGGGATTAATAATATGCTGAGTGATTTCCATGCAATGCTTGCTGTG	977
OY	250	-----MetAsnSerGlnValSerLeuIle	257
DB	978	GATAACCTGCAGATTTAAGAAATAATGAGACTCTAAACCACTGATGTGCTTCAACTT	1037
OY	258	GluArgAsnAlaPheAsnGlyLeuAlaSerLeuValGluLeuAsnLeuAlaHisAsnAsn	277
DB	1038	CACCCCATGATTTTTCAGACTGCCACAGGTGAATATCATCATGCTGAACACGCAATGCT	1097
OY	278	LeuSerSerLeuProHisAsnLeuPheThrProLeuArgTyrLeuValGluLeuHisLeu	297
DB	1098	CTCAGTGCCTGTACACATGATACCATGATGAGCTCTGCCAAACCTCAAGAAATACGACATA	1155
OY	298	HisHisAsnProTyrAsnCysAspCysAsnIleLeuTrpLeu-----AlaTrpTrp	314
DB	1158	CACAGTAAACCCATCAGGTGAGCTGTGTATCTCGTTGGATGAACATGAACAAACCAAC	1211
OY	315	LeuArgGluTyrIleProThrAsnSerThrCysGlyArgCysHisAlaProMetHis	334
DB	1218	ATTGAGATTTCATGAGCCAGCATCTACTGTTTGGCGTGAAC-----CACCTGAA	1265
OY	335	MetArgGlyArgTyrLeuValGluValAsp---GlnAlaSerPheGlnCysSerAlaPro	353
DB	1266	TTCCAGAGTCAAGATGTTCCGCAAGCTGATTTCAAGGACATGATGAATTTGTCTCCCT	1325
OY	354	PheIleMet-----AspAlaProArgAsnLeuAsnIleSerGluGlyArgMetAlaGlu	371

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Db      1326 CTTATAGCTCCTGAGAGCTTTCCTTCTATCTAAATGATGAGAGCTGGAGCTATGTTCC 1385
Qy      372 LeuysCyArg-----ThrProMetSerSerValysrTrpLeuLeuProAsnGly 389
Db      1386 TTTCAGTGTAAAGCTACTGACAGAACCAAGCTGAAATCTAGTGAATACACTTCTGGT 1445
Qy      390 ThrValLeuSerHisAlaSerArgHisProArgIleSerValLeuAsnAspGlyThrLeu 409
Db      1446 CAATAACTCTTGCCATATACCTGACAGACAAAGTCTATGTCATCTTGAGAGAAACACTA 1505
Qy      410 AsnPheSerHisValLeuLeuSerAspThrGlyValIlyThrCysMetGlyThrAsnVal 429
Db      1506 GATATTAATGCGCTAACTCCCAAGAGAGGGGTATATACTGATGATGCAACTAACCTA 1565
Qy      430 AlaGlyAsnSerAsnAlaSerAlaTyrLeu-----AsnGlySerThrAlaGluLeuAsn 447
Db      1566 GTTGCGCTGACTGAGCTGTATGATCAAGTGAATGATCTTTTCCACAGATAAC 1625
Qy      448 ThrSerAsnTyrSerPhePheThrThrGlyThrGlyIuThrThrGluIleSerProGlu 1667
Db      1626 AATGCTCTTGAATAT-----AAATRAAGATATTCAGGCCAAT 1667
Qy      468 AspThrThrArgLysTyrLys-----ProValProThrThrSerThrGlyTyrGln 484
Db      1668 TCAGTTTGCTGTCTCGTGAAGAGCAAGTCTTAATAATCTCAATCTAGTGAATGAGACA 1727
Qy      485 ProAlaTyrThrThrSerThrThrValLeuIleGlnThrThrArgValProLysGlnVal 504
Db      1728 GCGTTTGTCAAGACTGAAATTTCTATGCTGCGCAAGAGTCTGAAATCAATCTGANTGC 1787
Qy      505 AlaVal-----ProAlaThrAsp 510
Db      1788 AAGGTAATATCTTACTCATCTGAAATCATCAACTGAG 1826

RESULT 14
US-09-191-647-1
; Sequence 1, Application US/09191647
; Patent No. 6046015
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/191,647
; EARLIER FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: 60/065,544
; EARLIER FILING DATE: 1997-11-14
; EARLIER APPLICATION NUMBER: 60/081,057
; EARLIER FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4758
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4575)
US-09-191-647-1

Alignment Scores:
Pred. No.: 1,61e-32 Length: 4758
Score: 399.00 Matches: 147
Percent Similarity: 34.85% Conservative: 52
Best Local Similarity: 25.74% Mismatches: 177
Query Match: 11.58% Indels: 195
DB: 3 Gaps: 15

US-09-991-053-10 (1-653) x US-09-191-647-1 (1-4758)

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Qy      26 AlaGlnValTrpIleLeuCysAlaAlaIleAlaAlaIleAsnAla----- 41
Db      3 GCGGCGGCTGGTGGAGATGCTGTGCTGCTGCGGGTATGCTGCGCATCTGAA 62
Qy      42 -----GlyProGlnAsnCyProSerValCysSerCysSerAsnIlnPheSerLys 59
Db      63 CAAGTGGACCCGAGCGCGTCCCGGCGAGTGTCTTGGCTCGGGC-----AGCACAGT 116
Qy      59 IValCysThrArgArgGlyIleuSerGluValProGlnGlyIleProSerAsnThrArgTy 79
Db      117 GGAATGTCAGGGGCTGGCGCTGCCAGCTGCCAGAGAAATATCCCGCAACACCGAGAG 176
Qy      79 rLeuAsnLeuMetCylubAsnAnilIleGlnMetIleGlnAlaAspThrPheArgHisLeuH 99
Db      177 ACTGATTTAAATGAATATAACATCAACAAGATTAACAAGACAGATTTGCTGGTCTTAG 236
Qy      99 eHisLeuGluValLeuGlnIleuGlyArgAnserIleArgGlnIleGluValGlyAlaPh 119
Db      237 ACATCTAAGAGTCTTACGCTTATGAGAAATTAAGATTAAGACCATTTAAAGAGAGCATT 296
Qy      119 eAsnGlyLeuAlaSerLeuSerThrLeuGluLeuPheAspAsnTrpLeuThrValIlePr 139
Db      297 CCAGATCTTAAAGAACTAGAGAGACTGCGTTTAAACAGAAATCACTTCAGCTGTTCC 356
Qy      139 oSerGlyAlaPheGluTrpLeuSerLysLeuArgGluLeuTrpLeuArgAsnProI 159
Db      357 TGAATGCTGTTCTTGGAGCTCGAGAGCTATACAGCTTGATCTAGTGAACCAAT 416
Qy      159 eGluSerIleProSerTyrAlaPheAsnArgValProSerLeuMetArgLeuAspLeuG 179
Db      417 TCAGGCAATCCCAAGAAAGCTTCCGCGGGCGAGTTGAATATAAATTTGCAACTG-- 474
Qy      179 YGluLeuLysLeuLeuGluTrpIleSerGluGlyAlaPheGluGlyLeuPheAsnLeu 199
Db      475 -GATTAACAACCAAGATCAAGCTGTATTGAAGATGGGCAATTCAGGCTCTCGGAGCTGGA 533
Qy      199 sTyrLeuAsnLeuGlyMetCysAsnIle-----LysAspMe 211
Db      534 AGTGCTCACTCTCAACAATACAAATTAACATTAAGACTTCTGTGGCAAGTTTCAACCATAT 593
Qy      211 tProAsnLeu----- 214
Db      594 GCGTAACTTAAGAAGCTTTGACCTGACATTCACAACCTGTATTGTGACCTGCCACTGGCC 653
Qy      215 -----ThrProLeuValGlyLeu----- 220
Db      654 CTGGCTCTCGAGCTGGCTTGGCAAAAGGCTTGGGTTGGTCTGTACACTAGTGTATGGG 713
Qy      220 ----- 220
Db      714 CCCCTCCCACTGAGAGGCGATATATGACCGAGGTTCAAAAAGCAAAATTTGTCTGACAG 773
Qy      220 ----- 220
Db      774 TGATGAGAGAAAGGTGACAGCATATTATGAGCTCTTCTGTAGTGTGGACCTGCC 833
Qy      220 ----- 220
Db      834 TGCGGCTGTACTGTGACAACAATATGCTAGTGTGCGGAAAGCTTCACTGAGAT 893
Qy      221 -----GluGluLeuGluMetSerGlyAsnHisPheProG 232
Db      894 CCCCAAAATCTTCCAGAGACCATCAAGAAATACGTTTGGAAACAGAACCAATCAAGT 953
Qy      232 uIleArgProGlySerPheHisGlyLeuSerSerLeuLysLeuTrpValMetAsnSe 252
Db      954 CATCCCTCTCGAGACTTCTTACCATATAAAGCTTGAAGCAATTAAGCTCGACCAATTA 1013
Qy      252 rGlnValSerLeuLeuGluArgAsnAlaPheAspGlyLeuAlaSerLeuValGluLeuAs 272
Db      1014 TCAGATCTCTGAATTCACCAAGATGCTTTCAGAGACTAGCTCTGAAATTCACCTGT 1073
Qy      272 nLeuAlaHisAsnAsnLeuSerSerLeuPro----- 282

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Db      1074 CCTTATGAAATAAATCAAGAACTCCCAAAAGTTATTGAGAGACTGTTTCCTT 1133
Qy      282 -----
Db      1134 ACAGCTCCTATTATTGANTGCCAACAAGATAACTGCTGGGTAGATGCTTTTCAGGA 1193
Qy      283 -----HisAspLeu-----
Db      1194 TCTCCCAACTTGAACCTTCTCTCCCTATATGACAAACAGCTTCAGACCATGCCCAAGG 1253
Qy      286 ----PheThrProLeuArgTyrLeuValGluLeuHisLeuHisAsnProThrAsnCy 304
Db      1254 GACCTTTTCACTCTTCTGGGCACTTCAAACTATGTCATTTGCCCCAGAACCCCTTTATTTG 1313
Qy      304 SAAPCyAspPrlLeuLeuPrlLeuValPrlPrlLeuArgGluTyrIleProThrAsn----- 322
Db      1314 TGACTGCGCATCTCAAGTGGCTAGCG-----GATTATCTCATACCAACCCCGAT 1361
Qy      323 -SerThrCysCysGlyArgCysHisAlaProMetHisMetCysArgGlyArgTyrLeuValG1 342
Db      1362 TGAGACCAAGTGTGCCCGCTTGCACACAGCCCGCCCGCTGGCAAAACAAAGATTTGACA 1421
Qy      342 uValAspGlnAlaSerPheGlnCysSer-----AlaProPheIleLeu 356
Db      1422 GATCAAAAGCAAGAAATTCGGTGTTCAGAGTACAGAGATTATGATCAAAATTAAGTGG 1481
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Db      1482 AGACTGCTTTGGCATCTGGCTGGCTGGCTGAA-----AAGTGTCCCTG 1523
Qy      376 -----ThrProMetSerSerValIysTyrLeuPrlLeuProAsnGlyThrValIle 392
Db      1524 TGAAGAACCAACAGTAATGCTCTTAATCAAAAGCTC-----AACAAATCCC 1571
Qy      392 uSerHisAlaSerArgHisProArgIleSerValLeuAsnAspGlyThrLeuAsnPheSe 412
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## RESULT 15

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US-09-540-245A-1
; Sequence 1, Application US/09540245A
; Patent No. 6270984
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Brose, Katja
; APPLICANT: Teasler-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,245A
; PRIOR APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4758
; TYPE: DNA
; ORGANISM: human
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (1)..(4575)
US-09-540-245A-1
Alignment Scores: 1.61e-32 Length: 4758
Pred. No.:

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Score: 399.00 Matches: 147
Percent Similarity: 34.85% Conservative: 52
Best Local Similarity: 25.74% Mismatches: 177
Query Match: 11.58% Indels: 195
DB: 3 Gaps: 15

US-09-991-053-10 (1-653) x US-09-540-245A-1 (1-4758)
Qy      26 AlaGlnValTyrPrlLeuLeuValAlaAlaAlaAlaSerAla----- 41
Db      3 GCGCGGCTGTGGCGAGATGCTGTCCCTGTGCGGGTGTAGCTGGCGATCTCGAA 62
Qy      42 -----Gly-ProGlnAsnCySerProSerValCysSerCysSerAsnGlnPheSerLysVa 59
Db      63 CAAGTGGCACCGGACCGGCGCGCGCGAGCTCTTGTGTCGGGC-----AGCACAGT 116
Qy      59 lValCysThrArgArgGlyLeuSerGluValProGlnGlyIleProSerAsnThrArgTyr 79
Db      117 GCACTGTCAAGGCGCTGGCGCTGGCGAGCGTGCAGAGAAATATCCCCGCAACCCGAGAG 176
Qy      79 rLeuAsnLeuMetGlnAsnAsnIleGlnMetIleGlnAlaAspThrPheArgHisLeuH1 99
Db      177 ACTGATTTAATGAAATTAACATCAACAAGATTACAGAACAGATTTGCTGCTTAG 236
Qy      99 sHisLeuGluValLeuGlnLeuGlyArgAsnSerIleArgGlnIleGluValGlyAlaPh 119
Db      237 ACATCTAAGAGTCTTCAAGCTTATGAGAAATTAAGTATAGACACCTTGAAGAGAGCAT 236
Qy      119 eAsnGlyLeuAlaSerLeuSerThrLeuGluLeuPheAsnThrPrlLeuThrValIlePr 139
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Db      357 TGAGTTCGCTGTTCTTGGACCTGCGAAGCTATACAGGCTGATCTCAGTAAACCAAT 416
Qy      159 eGlnSerIleProSerTyrAlaPheAsnArgValProSerLeuMetCysLeuAspLeuG1 179
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Db      1524  TGAGGAACCAACAGTAGATTGCTTAATCAAAAGCTC-----AACAAATCCC 1571
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Db      1620  ATTTACCGTGTGGAAAGCCACAGAAATCTTT 1650

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 Job time : 155 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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(without alignments)  
4054.575 Million cell updates/sec

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
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Searched: 2356869 segs, 1788235258 residues  
Total number of hits satisfying chosen parameters: 4713738

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database :

Published Applications NA.\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query	Score	Match	Length	DB	ID	Description
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2	3446	100.0	2341	11	US-09-957-187-9	Sequence 9, Appl
3	3407	98.9	1962	13	US-10-203-708-2	Sequence 2, Appl
4	3407	98.9	2185	9	US-09-989-722-228	Sequence 228, App
5	3407	98.9	2185	9	US-09-989-723-228	Sequence 228, App
6	3407	98.9	2185	9	US-09-989-729-228	Sequence 228, App
7	3407	98.9	2185	9	US-09-989-727-228	Sequence 228, App
8	3407	98.9	2185	10	US-09-989-731-228	Sequence 228, App
9	3407	98.9	2185	10	US-09-989-732-228	Sequence 228, App
10	3407	98.9	2185	10	US-09-989-730-228	Sequence 228, App
11	3407	98.9	2185	10	US-09-990-442-228	Sequence 228, App
12	3407	98.9	2185	10	US-09-991-163-228	Sequence 228, App
13	3407	98.9	2185	10	US-09-993-604-228	Sequence 228, App
14	3407	98.9	2185	10	US-09-990-456-228	Sequence 228, App
15	3407	98.9	2185	10	US-09-989-721-228	Sequence 228, App
16	3407	98.9	2185	10	US-09-992-598-228	Sequence 228, App
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25	3407	98.9	2185	11	US-09-997-653-228	Sequence 228, App
26	3407	98.9	2185	11	US-09-993-667-228	Sequence 228, App
27	3407	98.9	2185	11	US-09-997-428-228	Sequence 228, App
28	3407	98.9	2185	11	US-09-997-666-228	Sequence 228, App
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37	3407	98.9	2185	11	US-09-997-573-228	Sequence 228, App
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41	3407	98.9	2185	11	US-09-997-601-228	Sequence 228, App
42	3407	98.9	2185	11	US-09-990-443-228	Sequence 228, App
43	3407	98.9	2185	11	US-09-991-854-228	Sequence 228, App
44	3407	98.9	2185	11	US-09-997-628-228	Sequence 228, App
45	3407	98.9	2185	11	US-09-997-683-228	Sequence 228, App

#### ALIGNMENTS

RESULT 1  
US-09-991-053-9  
Sequence 9, Application US/0991053  
Publication No. US20030003532A1  
GENERAL INFORMATION:  
APPLICANT: Shinkners, Richard A.  
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES ENCODING HUMAN SLIT-,  
FILE REFERENCE: 15966-540 CON S-10  
CURRENT APPLICATION NUMBER: US/09/991,053  
CURRENT FILING DATE: 2002-05-23  
PRIOR APPLICATION NUMBER: US95 60/123,667  
PRIOR FILING DATE: 1999-03-09  
PRIOR APPLICATION NUMBER: 09/520,781  
NUMBER OF SEQ ID NOS: 81  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 9  
LENGTH: 2341  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (215)..(2173)

US-09-991-053-9

## Alignment Scores:

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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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US-09-991-053-10 (1-653) x US-09-991-053-9 (1-2341)

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QY 21 PheValIYrLeuThrAlaGlnValTTPIleLeuCyAsnAlaIleAlaAlaAsn 40
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QY 41 AlaGlyProGlnAsnCyAsnProSerValCySerCySerAsnGlnPheSerIleVal 60
Db 335 GCCGGGCCCAAGAACTGCCCTCCCTCTGCTGTGACATACCACTTACAGAGTGTG 394

QY 61 CysThrArgArgIYLeuSerGluValProGlnGlyIleProSerAsnThrArgTyrLeu 80
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QY 81 AsnLeuMetGluAsnAsnIleGlnMetIleGlnAlaAspThrPheArgHisLeuHis 100
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QY 101 LeuGluValLeuGlnLeuGlyYArgAsnSerIleArgGlnIleGluValAlaPheAsn 120
Db 515 CTGAGAGCTCTGCAATTTGGGAGAGAACTCCATCCGCAAGATTGAGTGGGGCTTCAAC 574

QY 121 GlyLeuAlaSerLeuSerThrLeuGlnLeuPheAsnProTyrLeuThrValIleProSer 140
Db 575 GGCCTGGCGAGCTGAGCACTCTGAGAGCTGTTCGAACTGGCTGACAGTACTCCCTAGC 634

QY 141 GlyAlaPheGluTyrLeuSerIleYLeuArgGluLeuTyrPheAlaArgAsnProIleLeu 160
Db 635 GGGGCTTTGAATACCTGTCCAAAGCTGGAGAGCTGTGGCTTCCGAAACAACCCCACTCAA 694

QY 161 SerIleProSerTyrAlaPheAsnArgValProSerLeuMetArgLeuAspLeuGly 180
Db 695 AGCAATCCCTCTTACGCTTCAACCGGGTCCCTCTCTCATGCGCTGAGCTTGGGGAG 754

QY 181 LeuIYsIYsLeuGluTyrIleSerGluGlyAlaPheGlnGlyLeuPheAsnLeuIYsTyr 200
Db 755 CTCAAGAGAGCTGAGATATATCTCTGAGGAGAGCTTTGAGGGGCTGTTCAACTCAAGTAT 814

QY 201 LeuAsnLeuGlyMetCysAsnIleYLeuAspMetProAsnLeuThrProLeuValGlyLeu 220
Db 815 CTGAACCTTGGGAGTGTGAAACATTAAACAAGCCCAATCTCAACCCCTGGTGGGGTGG 874

QY 221 GluGluLeuGluMetSerGlyYAsnHisPheProGlnIleArgProGlySerPheHisGly 240
Db 875 GAGAGAGCTGAGATTCAGGAAACCACTTCCCTGAGATCAAGGCTGGCTCTCTCATGGC 934

QY 241 LeuSerSerLeuYsIYsLeuTyrValMetAsnSerGlnValSerLeuIleGluYArgAsn 260
Db 935 CTGAGACTCCCTCAAGAGCTGTGGGTCAATGAACCTCAAGGTCAAGCTAATTGAGGGAAT 994

QY 261 AlaPheAspGlyLeuAlaSerLeuValGluLeuAsnLeuAlaHisAsnAsnLeuSerSer 280
Db 995 GCTTTTGAAGGCTGGCTTCACTTGTGAACTCAACTGGCCCAATAATACCTCTCTCTCT 1054

QY 281 LeuProHisAspLeuPheThrProLeuArgTyrLeuValGluLeuHisLeuHisAsn 300
Db 1055 TTGCCCCATGACCTTTTACCCCGCTGAGGATCTGGTGGAGATTGTCACTTACACCAAC 1114

QY 301 ProTyrAsnCyAspCyAspIleLeuTyrPheAlaTyrTyrPheArgGluTyrIlePro 320

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Db 1115 CCTTGAACCTGTGATTGTGACCTTGTGGCTACCTGGTGGCTTCCAGAGTATATACCC 1174

QY 321 ThrAsnSerThrCysCySgIYArgCyAsnIleAlaProMetHisMetArgIYArgTyrLeu 340
Db 1175 ACCAATTTCCACTCTCTGTGGCCGCTGTCAATGTCTCCATGCAATGCAAGGGCCGTACTTC 1234

QY 341 ValGluValAspGlnAlaSerPheGlnCySerAlaProPheIleMetAspAlaProArg 360
Db 1235 GTGAGAGTGAACGAGGCTCTCTTCCAGTGTCTGCCCCCTTCATCATGAGCACTCGA 1294

QY 361 AspLeuAsnIleSerGlnGlyYArgMetAlaGluLeuYsCyAsnArgThrProProMetSer 380
Db 1295 GACCTCAACATTTCTGAGGGTGGATGCAAGAACTTAAAGTGTGCGACTCCCTCATATGTCC 1354

QY 381 SerValIYsTyrPheLeuProAsnGlyTyrValLeuSerHisAlaSerArgHisProArg 400
Db 1355 TCCGTAAAGTGTGCTGCTCCCAATGGACAGTGTCTACGCAAGCTCCGCAACCAAGG 1414

QY 401 IleSerValLeuAsnAspGlyTyrLeuAsnPheSerHisValLeuLeuSerAspThrGly 420
Db 1415 ATCTCTGTCTCAACGACGAGCACTTGAATTTCCACAGTGTGCTTTACAGACATGGG 1474

QY 421 ValIYrThrCyMetGlyThrAsnValAlaGlyAsnSerAsnAlaSerAlaTyrLeuAsn 440
Db 1475 GTGTACACATGCAATGGGAGCAATGTGACAGGCAACTCCAAAGCTCGGCTACTCAAT 1534

QY 441 GlySerThrAlaGluLeuAsnThrSerAsnTyrSerPhePheThrThrGlyGlu 460
Db 1535 GGGAGCAAGGCTGAGCTTAAACCTTCAACTCAAGCTTCTTACACAGGAACGGGGAG 1594

QY 461 ThrThrGlnIleSerProGlnAspThrThrArgIYsTyrIYsProValProThrThrSer 480
Db 1595 ACCACGAGATCTGTGCTGAGAGACACAACGGAAGTAAAGCTGTTCCTACACAGTCC 1654

QY 481 ThrGlyTyrGlnProAlaIYrThrThrSerThrThrValLeuIleGlnThrArgVal 500
Db 1655 ACTGTTACACGCGGAGATATACCACTTACCAAGGTGTCTCATCAGACTACCGGTGTG 1714

QY 501 ProIYsGlnValAlaValProAlaThrAspThrThrAspIYsMetGlnThrSerLeuAsp 520
Db 1715 CCCAAGAGGTGGAGTACCCGCAACACCACTCAACAGATGACAGACCAAGCTGGAT 1774

QY 521 GluValMetIYsTyrThrIYsIleIleIleGlyCysPheValAlaValThrLeuLeuAla 540
Db 1775 GAACTCATGAAGACCAACAAGATCATATGGCTGTGTGGAGAGACTGTGCTAGCT 1834

QY 541 AlaAlaMetLeuIleValPheTyrIYsLeuArgIYsArgHisGlnIYsArgSerThrVal 560
Db 1835 GCCGCCATGTGATGTCTTCTTAACCTTGTAAAGCGGCAACGAGCGAGTACAGTC 1894

QY 561 ThrAlaIaArgThrValGluIleIleGlnValAspGluAspIleProAlaIaThrSer 580
Db 1895 ACAGCCCGCGAGCTGTGAGATATCCAGTGGACGAAGACATCCGACGCAACATCC 1954

QY 581 AlaAlaIaThrAlaIaProSerGlyValSerGlyGlnGlyAlaValIleuProThr 600
Db 1955 GCACACCAACAGACAGCTCCGTCGGTGTATCAGTGAAGGGAGAGTGTCTGCCACA 2014

QY 601 IleHisAspHisIleAsnTyrAsnThrTyrIYsProAlaHisGlyAlaHisTyrThrGlu 620
Db 2015 ATTCATGACCATATTATTACTCAACAACCTCAACAACAGACATGGGGCCCACTGACAGAA 2074

QY 621 AsnSerLeuGlyAsnSerLeuHisAspThrValThrThrIleSerGluProTyrIleIle 640
Db 2075 AACAGCTTGGAGACTCTGTGACCCCAAGTACCACTATCTCTGAACCTTATATATT 2134

QY 641 GlnThrHisThrIYsAspIYsValGlnGluThrGlnIle 653
Db 2135 CAGACCATACCAAGGACCAAGTACAGAAACTCAATA 2173

RESULT 2
US-09-957-187-9

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Db 1775 GAAGTCATGAAGACCAACAGATCATCTGCTGCTTGGCAGTACTGCTGCTACT 1834  
 Qy 541 A1A1A1Me1Leu1Leu1Val1Phe1Ty1Leu1Arg1Val1Gln1Gln1Arg1Ser1Thr1Val 560  
 Db 1835 GCCCGCATGTTGATTTGTTCTTCTTAACTTCTGTAAGCCGACACAGCAGGAGTACATC 1894  
 Qy 561 Thr1Ala1Arg1Thr1Val1Glu1Leu1Leu1Val1Arg1Leu1Pro1Ala1Ala1Ser 580  
 Db 1895 ACAGCCGCCGAGCTGTTGAGATATATCCAGGTGACGAAGACATCCAGCAGCAACATCC 1954  
 Qy 581 A1A1A1A1A1Thr1Ala1Ala1Pro1Ser1Val1Ser1Glu1Glu1Val1Ala1Val1Leu1Pro1Thr 600  
 Db 1955 GCACAGACGAACAGCAGCTCTCTGCAACCCACAGTCAACATATCTGAACTTATATATT 2134  
 Qy 601 I1Leu1Asp1His1Leu1Ser1Val1Ser1Glu1Glu1Val1Ala1Ala1Ser1Thr1Glu 620  
 Db 2015 ATTCTATGACCATTTATTAATTAACACCTTAACACACAGACATGGGGCCCATCTGACAGAA 2074  
 Qy 621 Aas1Ser1Leu1Glu1Aas1Ser1Leu1His1Pro1Thr1Val1Thr1His1Ser1Glu1Pro1Ty1Leu1 640  
 Db 2075 AACAGCCTGGGGAACCTCTCTGCAACCCACAGTCAACATATCTGAACTTATATATT 2134  
 Qy 641 G1n1Thr1His1Thr1Val1Asp1Val1Gln1Gln1Leu1Gln1Leu1 653  
 Db 2135 CAGACCATACCAAGACAGATACAGAACTCAATA 2173

# RESULT 3

US-10-203-708-2  
 : Sequence 2, Application US/10203708  
 : Publication No. US20030149238A1  
 : GENERAL INFORMATION:  
 : APPLICANT: SMITHKLINE BEECHAM CORPORATION  
 : TITLE OF INVENTION: NOVEL COMPOUNDS  
 : FILE REFERENCE: G950013  
 : CURRENT APPLICATION NUMBER: US/10/203,708  
 : PRIOR FILING DATE: 2002-08-13  
 : PRIOR APPLICATION NUMBER: PCT/US01/04703  
 : PRIOR FILING DATE: 2001-02-14  
 : PRIOR APPLICATION NUMBER: 60/182,172  
 : PRIOR FILING DATE: 2000-02-14  
 : PRIOR APPLICATION NUMBER: 60/186,084  
 : NUMBER OF SEQ ID NOS: 46  
 : SOFTWARE: FASTSEQ for Windows Version 3.0  
 : SEQ ID NO 2  
 : LENGTH: 1962  
 : TYPE: DNA  
 : ORGANISM: Homo sapiens  
 : US-10-203-708-2

## Alignment Scores:

Pred. No.: 0 Length: 1962  
 Score: 3407.00 Matches: 648  
 Percent Similarity: 99.39% Conservative: 1  
 Best Local Similarity: 99.23% Mismatches: 4  
 Query Match: 98.87% Indels: 0  
 DB: 13 Gaps: 0

US-09-991-053-10 (1-653) x US-10-203-708-2 (1-1962)

Qy 1 Met1Val1Leu1Leu1Trp1Gln1Val1Thr1Val1His1His1Thr1Pro1Ala1Ala1Leu1Leu1Pro 20  
 Db 1 ATGAAGCTCTTGTGGCAGGTAACTGTGACACCAACCACTGGAATGCAATCTGTCTCCG 60  
 Qy 21 Phe1Val1Trp1Leu1Thr1Ala1Gln1Val1Trp1Leu1Cys1Ala1Ala1Ala1Ala1Ser 40  
 Db 61 TTCGTCATCTCAAGCGGCAAGTGTGATTCGTGTGTGACGATGCTGCTGCCGCTCA 120  
 Qy 41 Ala1Gly1Pro1Gln1Aas1Pro1Ser1Val1Cys1Ser1Cys1Ser1Aas1Gln1Phe1Ser1Val1Val 60  
 Db 121 GCCGGGCCCCAGAACTGCCCTCCCTCTGCTCTGTGACATTAACAGTTACGACGAAGGTG 180

Qy 61 Cys1Thr1Arg1Arg1Leu1Ser1Glu1Val1Pro1Gln1Glu1Leu1Pro1Ser1Aas1Thr1Arg1Trp1Leu 80  
 Db 181 TGACAGCGCGCGGAGCTCTCCAGAGTCCCGAGAGGTATTCCTCTGAACACCCGGTACTC 240  
 Qy 81 Aas1Leu1Met1Glu1Aas1Aas1Ile1Gln1Met1Ile1Gln1Ala1Asp1Thr1Phe1Arg1Ile1His1His 100  
 Db 241 AACCTCATGAGAAACAACATCCAGATATCCAGGCCACACACCTTCCCGCACCTCCACAC 300  
 Qy 101 Leu1Glu1Val1Leu1Gln1Glu1Arg1Aas1Ser1Ile1Arg1Gln1Ile1Glu1Val1Ala1Phe1Asn 120  
 Db 301 CTGAGAGTCTCTGCACTTGGGAGGAATCTCATCCGACAGATTAAGTGGGGGCTTTAC 360  
 Qy 121 G1Leu1Ala1Ser1Leu1Ser1Thr1Leu1Glu1Leu1Phe1Asp1Aas1Thr1Val1Ile1Pro1Ser 140  
 Db 361 GGCCTGGCCAGCTCAACACCTGAGCTGTGCAACATGGCTGACAGTCACTCACTTAC 420  
 Qy 141 G1Val1Ala1Phe1Glu1Trp1Leu1Ser1Val1Arg1Glu1Leu1Trp1Leu1Aa1Aas1Pro1Ile1Glu 160  
 Db 421 GGGGCTTTGAAATACCTGTCACAGCTGGGAGCTTGGCTTGGCAACACCCCATGAA 480  
 Qy 161 Ser1Ile1Pro1Ser1Trp1Ala1Phe1Aas1Arg1Val1Pro1Ser1Leu1Met1Arg1Leu1Asp1Leu1Glu 180  
 Db 481 AGCATCCCTCTTACGCTCTTACACCGGAGTCCCTCTCATGCGCTGGACTTGGGGAG 540  
 Qy 181 Leu1Val1Ser1Leu1Glu1Trp1Ile1Ser1Glu1Ala1Phe1Glu1Leu1Phe1Asn1Leu1Val1Ser1 200  
 Db 541 CTCAGAAAGCTGAGATATCTCTGAGGAGCTTTTAAAGGGGCTTCAACCTCAAGTAT 600  
 Qy 201 Leu1Aas1Leu1Glu1Met1Cys1Aas1Ile1Val1Asp1Met1Pro1Aas1Leu1Thr1Pro1Leu1Val1Glu 220  
 Db 601 CTGAACCTTGGGAGCTGTCACACATTAAGACATGCCCAATCTCAACCCCTGGTGGGCTG 660  
 Qy 221 G1n1Glu1Leu1Glu1Met1Ser1Glu1Aas1His1Phe1Pro1Glu1Ile1Arg1Pro1Glu1Ser1Phe1His1Gly 240  
 Db 661 GAGGAGCTGGAGATGTAGGAGAACCTTCTCTGAGTCAAGGCTGCTCTCTCTCATAGCC 720  
 Qy 241 Leu1Ser1Ser1Leu1Val1Ser1Leu1Trp1Val1Met1Aas1Ser1Gln1Val1Ser1Leu1Ile1Glu1Arg1Asn 260  
 Db 721 CTGAGCTCCCTCAAGAAAGCTCTGGGTCATGAATCAACAGGTACAGCTGATTAAGCGGAT 780  
 Qy 261 Ala1Phe1Asp1Glu1Leu1Ala1Ser1Leu1Val1Glu1Leu1Aas1Leu1Ala1His1Aas1Aas1Leu1Ser1Ser 280  
 Db 781 GCCTTTACCGGCGGCTTCACTTGTGAACTCAACTGGCCCAATAACTCTCTCTCT 840  
 Qy 281 Leu1Pro1His1Asp1Leu1Phe1Thr1Pro1Leu1Arg1Trp1Leu1Val1Glu1Leu1His1His1Asp 300  
 Db 841 TTGCCCATGACCTCTTACCCGCTGAGGATCTGGAGGTGACATCTACACACACAC 900  
 Qy 301 Pro1Trp1Aas1Cys1Asp1Cys1Asp1Ile1Leu1Trp1Leu1Ala1Trp1Leu1Arg1Glu1Trp1Ile1Pro 320  
 Db 901 CTTTGAAGCTGTATTTGTGACATTTCTGTGGTACCTGTGGCTTGCAGAGTATATATACC 960  
 Qy 321 Thr1Aas1Ser1Thr1Cys1Cys1Glu1Arg1Cys1His1Ala1Pro1Met1His1Met1Arg1Val1Arg1Trp1Leu 340  
 Db 961 ACCAAATTCACCTGCTGTGGCCGCTGTCATGCTCCCAATGACATGACAGGCGGCTTACTC 1020  
 Qy 341 Val1Glu1Val1Asp1Gln1Ala1Ser1Phe1Gln1Cys1Ser1Ala1Pro1Phe1Ile1Met1Aa1Ala1Pro1Arg 360  
 Db 1021 GTGAGAGTGAACAGGCTCTCTTCAAGTGTCTGCCCCCTTCACTCATGAGACGACCTTGA 1080  
 Qy 361 Asp1Leu1Aas1Ile1Ser1Glu1Arg1Met1Ala1Glu1Leu1Val1Cys1Arg1Thr1Pro1Met1Ser 380  
 Db 1081 GACCTCAACATTTCTGAGGCTCGGATGGCAGAACTTAAGTGTGCAATCTCCCTATATGCC 1140  
 Qy 381 Ser1Val1Ile1Trp1Leu1Leu1Pro1Aas1Glu1Thr1Val1Leu1Ser1His1Ala1Ser1Arg1His1Pro1Arg 400  
 Db 1141 TCCGTGAAGGTGTGCTGCCCAATGGGACAGTGTCAAGCACGCTCCCGCACCAAGG 1200  
 Qy 401 Ile1Ser1Val1Leu1Aas1Pro1Glu1Trp1Leu1Aas1Phe1Ser1Ile1Val1Leu1Ser1Asp1Thr1Gly 420  
 Db 1201 ATCTCTGTCTCAACAGCGACCTTGAACCTTTTCCACAGTGTGCTTTTACAGACACTGGG 1260  
 Qy 421 Val1Trp1Thr1Cys1Met1Glu1Thr1Aas1Val1Ala1Glu1Aas1Ser1Aas1Ala1Ser1Ala1Trp1Leu1Aas1 440



Db 1261 GTGACACATGATGAGTACCAAGTGCAGGCACTCCAGCCTGAGCTTACTCAAT 1320  
Qy 441 GlySerThrIleuAsnThrSerAsnTyrSerPhePheThrGlyThrGlyGlu 460  
Db 1321 GTGAGCAGGCTGAGCTTAACCTCCACACTACAGCTTCTTCCACACAGTACGAG 1380  
Qy 461 ThrThrGluIleSerProGluAspThrThrArgIleTyrIleProValProThrThrSer 480  
Db 1381 ACCACGAGATCTGCTGAGGACACACGAGAAAGTACAGCTGTCTTCCACACAGCTCC 1440  
Qy 481 ThrGlyTyrGlnProAlaTyrThrThrSerThrValIleuIleGlnThrThrArgVal 500  
Db 1441 ACTGGTACACAGCCGCGATATACCACTTACCAAGGTGCTCATTCAGACTACCGCTGAG 1500  
Qy 501 ProIleGlnValAlaValProAlaThrAspThrThrAspIleMetGlnThrSerLeuAsp 520  
Db 1501 CCCAAGCAGGTGGAGTACCCGCGACAGACCACTGACAGATGACAGACCGCTGAT 1560  
Qy 521 GluValMetIleThrThrIleIleIleGlyCysPheValAlaValThrLeuAla 540  
Db 1561 GAAGTATGAAGACCAACAGATCATTCGCTGCTTTGGCAGTGCATCTGCTAGCT 1620  
Qy 541 AlaAlaMetIleuIleValPheTyrIleuArgIleArgIleGlnArgSerThrVal 560  
Db 1621 GCCGCGCATGTTGATGTTCTTATAAATTCTGTAAGCGGCACGACGAGGAGTACAGTC 1680  
Qy 561 ThrAlaIleArgThrValGluIleIleGlnValAspGluAspIleProAlaThrSer 580  
Db 1681 ACAGCCCGCGAGCTGTGATATATCAGGTGACAGACATCCACAGCAGCAATCC 1740  
Qy 581 AlaAlaIleThrAlaIleProSerGlyValSerGlyGluGlyAlaValIleuProThr 600  
Db 1741 GCAGCAGCAACAGACGCTCCCTCCGCTGTATCAGTGAAGGAGGAGTGTCTCCACA 1800  
Qy 601 IleIleAspHisIleAsnTyrAsnThrTyrIleProAlaHisGlyAlaHisIleProThrGlu 620  
Db 1801 ATTCAATGACCATATTAACTACCAACACCTACCAACAGACATGGGGCCACTGCACGAA 1860  
Qy 621 AsnSerIleuGlyAsnSerIleuHisProThrValThrThrIleSerGluProTyrIleIle 640  
Db 1861 AACCGCTGGGAACTCTGACACCCACCACTCCACTCACTCTGAACCTATATATATT 1920  
Qy 641 GlnThrIleThrIleAspIleValGlnGluThrGlnIle 653  
Db 1921 CAGACCATACCAAGACAGGTACAGGAATCTAATA 1959

APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C63  
CURRENT APPLICATION NUMBER: US/09/989,722  
PRIOR FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
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 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091978  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.: 0 Length: 2185  
 Score: 3407.00 Matches: 648  
 Percent Similarity: 99.39% Conservative: 1  
 Best Local Similarity: 99.23% Mismatches: 4  
 Query Match: 98.87% Indels: 0  
 DB: 9 Gaps: 0

US-09-991-053-10 (1-653) x US-09-989-722-228 (1-2185)

QY 1 MetLysLeuLeuTrpGlnValThrValHisHisThrTrpAsnAlaIleLeuLeuPro 20  
 DB 57 ATGAAGCTCTTGTCGAGTAACTGTGACACACACCTGAATGCCATCTCTCCG 116  
 QY 21 PheValTyrLeuThrAlaGlnValTrrIleLeuCysAlaAlaIleAlaAlaSer 40  
 DB 117 TTCCTTCACTCCACGGCGCAAGTGTGATTCTGTGCACCACTGCTGCGCTCA 176  
 QY 41 AlGdlYProGlnAsnCysProSerValCysSerCysSerAsnGlnPheSerLysVal 60  
 DB 177 GCCGGGCCCCAGAACTCCCTCCGTTGCTGTGACGTAAACAGTTCAGCAAGTGTG 236  
 QY 61 CysThrArgArgGlyLeuSerGluValProGlnGlyIleProSerAsnThrArgTyrLeu 80  
 DB 237 TGACAGCGCGCGGCGCTCTCCAGAGTCCCGCAGGATATTCCTCGAACACCCGGTACTC 296  
 QY 81 AsnLeuMetGluAsnAniIleGlnMetIleGlnAlaAspThrPheArgHisIleHis 100  
 DB 297 AACCTCATGAGAACATCCAGATGATCAGAGCCGACACTTCCGCCACTTCACACAC 356  
 QY 101 LeuGluValLeuGlnLeuGlyArgAsnSerIleArgGlnIleGluValGlyAlaPheAsn 120  
 DB 357 CTGAGGCTCTGCACTGGGAGGAGAACTCATCCGAGATTGAGTGGGCGCTTCAC 416  
 QY 121 GlyLeuAlaSerLeuSerThrLeuGluLeuPheAspAsnTrpLeuThrValIleProSer 140  
 DB 417 GGCTGGCCAGCTCAACACCTGGAGCTGTGACAACTGGCTGACAGTCATCTTACG 476  
 QY 141 GlyAlaPheGluTyrLeuSerLysLeuArgGluLeuTrrLeuArgAsnAsnProIleGlu 160  
 DB 477 GGGGCTTTGAATTAATCTGTCAAGAGCTGGGAGCTGTGCTTGCCAAACCCCATGAA 536

QY 161 SerIleProSerTyraIaPheAsnArgValProSerLeuMetArgLeuAspLeuGlu 180  
 DB AGCATCCCTTACCGCTTCAACCGGGTGCCTCCCTCATGCGCTGAGACTGGGGAG 596  
 QY 181 LeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 200  
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 QY 201 LeuAsnLeuGlyMetCysAsnIleValAspMetProAsnLeuThrProLeuValGlyLeu 220  
 DB CTGAACCTGGGCACTGTCACCACTTAAAGACATGCCCAATCTCAACCCCTGGTGGGCTG 716  
 QY 221 GluGluLeuGluMetSerGlyAsnHisPheProGluIleArgProGlySerPheHisGly 240  
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 QY 241 LeuSerSerLeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 260  
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 QY 261 AlaPheAspGlyLeuAlaSerLeuValGluLeuAsnLeuIleHisAsnLeuSerSer 280  
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 DB GACCTCAACATTTCTGAGGGTGGGATGAGCAACTTAAAGTCTGCACTCCCTATATGCTC 1196  
 QY 381 SerValIleThrLeuLeuProAsnGlyThrValLeuSerHisAlaSerArgHisProArg 400  
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 DB ATCTCTCTCTCAACGACGAGCCTTGAATCTTTCCACGCTGCTCTTTCAGACACTGGG 1316  
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 DB GTGAGCACGCTGAGTAACTCACTCAACGCTCTTCAACCAAGTAAAGTGGAG 1436  
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 QY 521 GluValMetIleThrThrIleIleIleGlyCysPheValAlaValThrLeuAla 540

DB 1617 GAAGCATGAGAGACCAACAGATCATGCTGCTTGTGCGACATGCTGCTGAGCT 1676  
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 QY 581 AlaAlaAlaThrAlaAlaProSerGlyValSerGlyGluIleValAlaValLeuProThr 600  
 DB 1797 GCAGACGACAAACAGACACTCCGCTCGGTATCAGTGAAGGGGACAGTGTGCGCACA 1856  
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 DB 1917 AACAGCTGGGGAATCTCTGACACCCACAGTACACATATCTCTGAACTTATATATT 1976  
 QY 641 GlnThrHisThrIleAspIleValGlnGluThrGlnIle 653  
 DB 1977 CAGACCATATCAAGAGCAAGTACAGAAATCAATA 2015  
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 RESULT 5  
 US-09-989-723-228  
 ; Sequence 228, Application US/09989723  
 ; Patent No. US20020072092A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerltsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Guiney, Austin L.  
 ; APPLICANT: Kijavlin, Ivar J.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2730P1C62  
 ; CURRENT APPLICATION NUMBER: US/09/989,723  
 ; PRIOR FILING DATE: 2001-11-19  
 ; PRIOR APPLICATION NUMBER: 60/049787  
 ; PRIOR FILING DATE: 1997-06-16  
 ; PRIOR APPLICATION NUMBER: 60/062250  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/065186  
 ; PRIOR FILING DATE: 1997-11-12  
 ; PRIOR APPLICATION NUMBER: 60/065311  
 ; PRIOR FILING DATE: 1997-11-13  
 ; PRIOR APPLICATION NUMBER: 60/066770  
 ; PRIOR FILING DATE: 1997-11-24  
 ; PRIOR APPLICATION NUMBER: 60/075945  
 ; PRIOR FILING DATE: 1998-02-25

[illegible]

PRIOR APPLICATION NUMBER: 60/091626  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091633  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091978  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.:	0	Length:	2185
Score:	3407.00	Matches:	648
Percent Similarity:	99.39%	Conservative:	1
Best Local Similarity:	99.23%	Mismatches:	4
Query Match:	98.87%	Indels:	0
DB:	9	Gaps:	0

US-09-991-053-10 (1-653) x US-09-989-723-228 (1-2185)

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 QY 21 PheValTyrleuThrAlaGlnValTrrlleuGlyAlaAlaIleAlaAlaSer 40  
 DB 117 TTGCTTCACTCAAGGCGCAAGTGTGATCTGTGTGACGCACTGCTGCGGCTCA 176  
 QY 41 AlaGlyProGlnAnuGlyProSerValCysSerCysSerAnuGlnPheSerValVal 60  
 DB 177 GCCCGGCGCCAGAACTGCCCTCCGTGTGCTGTGAGTAACAGTTCAGCAAGGTGGT 236  
 QY 61 CysThrArgArgGlyLeuSerGluValProGlnGlyIleProSerAnuThrArgTyrleu 80  
 DB 237 TGCAGCGCGCGGCGCTCTCGAGAGTCCCGAGGATATCCCTGAAACACCGGCTACCTC 296  
 QY 81 AsnleuMetGluAnuAnuIleGlnMetIleGlnAlaSerThrPheArgHisIleuHis 100  
 DB 297 AACCTCATGAGAAACATCATCATCATCATCATCATCATCATCATCATCATCATCAT 356  
 QY 101 LeuGluValleuGlnleuGlyArgAsnSerIleArgGlnIleGluValGlyAlaPheAsn 120  
 DB 357 CTGAGAGGCTGAGTGTGGGAGGAACTCCATCCGGAGATGAGTGGGGGCTTCAAC 416  
 QY 121 GlyleuAlaSerleuSerThrleuGluLeuPheAsnThrIleProSer 140  
 DB 417 GGCCTGCGACGCTCAACACCTGAGGCTGTTCACAACTGGCTGACATCATCATCAT 476  
 QY 141 GlyAlaPheGluTyrleuSerIleValArgGluTyrleuAlaGlyAnuProIleGlu 160  
 DB 477 GGGGCTTTGAAATCTGCTCAACAGCTCGGAGAGCTGTGCTTCCGAACACCCATCGAA 536  
 QY 161 SerIleProSerTyrAlaPheAsnArgValProSerleuMetArgleuAspIleGlu 180  
 DB 537 AGCATCCCTCTTACGCTTCAACCGGGTGCCTCCCTCAAGGCTGGAATTGGGGAG 596  
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 DB 657 CTGAACCTTGGGAGCTGCAACATTAACATGCGCAATCTCAACCCCTGAGGGCTG 716  
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 DB 717 GAGAGCTGAGATGTGAGGAAACCTTCCCTGAGATCAAGCTGCTCTTCCATGCG 776  
 QY 241 LeuSerSerleuIlySylleuTyrValMetAnuSerGlnValSerleuIleGluArgAnu 260  
 DB 777 CTGAGCTCCCTCAAGAAAGCTGTGGGTCAAGAACTCAAGGTCAAGCTGATTAAGCGGAA 836

QY 261 AlaPheAspGlyleuAlaSerleuValGluLeuAnuLeuAlaHisAnuAnuLeuSerSer 280  
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 DB 897 TTGCGCATGACCTTTTACCGCGTGAAGTACCTGTGTGAGTGTGATCTTCAACAC 956  
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 QY 341 ValGluValAspGlnAlaSerPheGlnCysSerAlaProPheIleMetAlaProArg 360  
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 DB 1137 GACCTCAACATTTCTAGAGGTGGATGGACAACTTAAGTGTGAACTCCCTATGTCC 1196  
 QY 381 SerValIlySerleuLeuProAnuGlyThrValleuSerHisAlaSerArgHisProArg 400  
 DB 1197 TCCGTAAAGTGTGCTGCCCCAATGGAGACGTCTACGCCACCTCCGCCACCAAG 1256  
 QY 401 IleserValleuAnuAnuGlyThrleuAnuPheSerHisValleuLeuSerAspThrGly 420  
 DB 1257 ATCTGTCTTCAACGACGCGCACCTTGAACTTTTCCACGCTGCTTTCAGACACTGGG 1316  
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 QY 461 ThrThrGluIleSerProGluAspThrThrArgIlySylleuProValProThrThrSer 480  
 DB 1437 ACCACGAGATCTCGCTGAGACACAAACGAAAGTCAAGCTGTCTTCAACAGTCC 1496  
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 DB 1497 ACTGTTACCAAGCGGATATACCACTTACCAAGGTGTCTCATTTCAAGCTACCGGTG 1556  
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 QY 561 ThrAlaAlaArgThrValGluIleIleGlnValAspGluAspIleProAlaAlaThrSer 580  
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Db 1917 AACGCGTGGGAACTCTCTCACCACAGTCAACACTATCTGAACTTATATATT 1976  
Cy 641 GlnthrhsthrlyAspIyVaIglnglnthrglnle 653  
Db 1977 CAGACCATACCAAGAGAGAGTACGGAAGAACTCAATA 2015

## RESULT 6

US-09-989-279-228 Application US/09989279  
Sequence 228. Application US/09989279  
Patent No. US20020072496A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deamovets, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlesen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, V. Christopher  
APPLICANT: Gurney, Aubelin L.  
APPLICANT: KJavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC56  
CURRENT APPLICATION NUMBER: US/09/989,279  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
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PRIOR FILING DATE: 1998-02-25  
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PRIOR FILING DATE: 1998-05-28  
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PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090246

PRIOR FILING DATE: 1998-06-22  
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 PRIOR FILING DATE: 1998-07-01  
 PRIOR APPLICATION NUMBER: 60/091519  
 PRIOR FILING DATE: 1998-07-02  
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 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091633  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091978  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.: 0  
 Score: 3407.00  
 Percent Similarity: 99.39%  
 Best Local Similarity: 98.87%  
 Query Match: 9  
 Gaps: 0

Length: 2185  
 Matches: 648  
 Conservative: 1  
 Mismatches: 4  
 Indels: 0

US-09-991-053-10 (1-653) x US-09-989-279-228 (1-2185)

QY	1	MetLysLeuLeuTrpGlnValThrValHisHisHisThrTrpAsnAlaIleLeuLeuPro	20
DB	57	ATGAAGCTCTTGGCAGAGTAACTGTGCACACCACTCGAATGCAATCTGCTCCG	116
QY	21	PheValTyrLeuThrAlaGlnValTyrIleLeuCysAlaAlaIleAlaAlaSer	40
DB	117	TTGCTTACTTCAACGGCGCAAGTGGATTCGTGTGACGCATCGCTGCTGCCCTCA	176
QY	41	AlaGlyProGlnIleCysProSerValCysSerCysSerAsnGlnPheSerValVal	60
DB	177	GCCGGGCCCAAGACTGCCCTCGTTGCTGTGAGTAAACCAATTCAGCAAGTGGTG	236
QY	61	CysThrArgArgIleLeuSerGlnValProGlnGlyIleProSerAsnThrArgTyrLeu	80
DB	237	TGCAACGGCCGGGGCTCTCCAGGTCCCGCAGAGTATTCCTTCAACACCGGTACTTC	296
QY	81	AsnLeuMetGlnAsnAsnIleGlnMetIleGlnAlaAspThrPheArgHisHis	100
DB	297	AACCTCATGGAACAACATCCAGATGATCCAGCCGACACCTTCGCCACCTCCACAC	356
QY	101	LeuGlnValLeuGlnLeuGlyArgAsnSerIleArgGlnIleGlnValGlyAlaPheAsn	120
DB	357	CTGAGAGTCTCGAGTGGCAGGAACCTCCATCCGACAGTGAAGTGGGGCTTCAAC	416
QY	121	GlyLeuAlaSerLeuSerThrLeuGlnLeuPheAspAsnThrLeuThrValIleProSer	140
DB	417	GGCCCTGGCCAGCTCAACACCTGAGCTGTGACCACTGGCTGACAGTCACTTCAGC	476
QY	141	GlyAlaPheGlnTyrLeuSerTyrLeuArgGlnLeuTyrLeuArgAsnProIleGln	160
DB	477	GGGGCCCTTTAATACCTGCTCAAGCTGGGAGACTCGCTTGGCAACAACCCCATGGA	536
QY	161	SerIleProSerTyrAlaPheAsnArgValProSerLeuMetArgLeuAspLeuGlyGln	180
DB	537	AGCATCCCTCTTACGCTTCAACCGGGTGCCTCTCCATCGCGCTTGGAGGAG	596
QY	181	LeuIleTyrLeuGlnTyrIleSerGlnGlyAlaPheGlnGlyLeuPheAsnLeuTyr	200
DB	597	CTCAAGAGCTGAGATGATCTCTGAGGAGCTTTTGAAGGGCTGTTCACCTCAAGTAT	656
QY	201	LeuAsnLeuGlyMetCysAsnIleTyrAspMetProAsnLeuThrProLeuValGlyLeu	220
DB	657	CTGAACCTGGGCACTGTCAACATTTAAAGACATGCCAATTCACCCCTGCTGGGCTG	716
QY	221	GlnGlnLeuGlnLeuSerGlyAsnHisPheProGlnIleArgProGlySerPheHisGly	240
DB	717	GAGGAGCTGAGATGTCAGGGAACCACTTCCGATGATCAGGCTGCTCCATGAGC	776
QY	241	LeuSerSerLeuTyrLeuTyrValMetAsnSerGlnValSerLeuIleGlnValArgAsn	260
DB	777	CTGAGCTCCCTCAAGAGCTCTGGTCAATGATCAAGGTGAGCTGATTTGAGCGAAT	836
QY	261	AlaPheAspGlyLeuAlaSerLeuValGlnLeuAsnLeuAlaHisAsnAsnLeuSerSer	280
DB	837	GCTTTTACCGGGCTGCTTACTTGTGAACTTAACCTTGGCCCAATTAACCTCTCTCT	896
QY	281	LeuProHisAspLeuPheThrProLeuArgTyrLeuValGlnLeuHisHisAsn	300
DB	897	TTGGCCCATGACCTCTTACCCCGGAGGTACTGGTGAAGTTGATTCACACCAAC	956
QY	301	ProTyrAsnCysAspCysAspIleLeuTyrLeuAlaTyrTyrLeuValGlyTyrIlePro	320
DB	957	CTTGAACCTGATTTGTGACATTTCTGTGCTGAGCTGAGGCTTCAGAGTATTAACCC	1016
QY	321	ThrAsnSerThrCysCysGlyArgCysHisAlaProMetHisMetArgGlyArgTyrLeu	340
DB	1017	ACCAATTTCCACTGCTGTGCGCGCTGTCATGCTCCATGACATGCGAGGCCGCTACTTC	1076
QY	341	ValGlnValAspGlnAlaSerPheGlnCysSerAlaProPheIleMetAspAlaProArg	360
DB	1077	GTGAGAGTGAACAGGCTCTTCCAGTGTCTGCGCCCTTCATCATGACGACCTCGA	1136

QY 361 AspleuanaIIleSerGIuIyArgMetAlaGluLeuIySvArgThProProWetSer 380  
 Db 1137 GACCTCAACATTTCTGAGGGTGGATGGAGAACTTAAGTGTGGACTCCCTTAATGTC 1196  
 QY 381 SerValIySTPLeuLeuProAsnGlyThrValIleuSerHISAlaSerArgHisProArg 400  
 Db 1197 TCCGGAAGAGTGTGCTCCCAATGGAGAGGTGCTGACCCACGCTCCCGGACCAAGG 1256  
 QY 401 ILeSerValIleuAsnAspGlyThrLeuAsnPheserHISValIleuSerAspThrGly 420  
 Db 1257 ATCTGTCTCTCAAGAGAGGACCTTGAACCTTTCCACGCTGCTCTTGAAGACTGG 1316  
 QY 421 ValIyThrCvMetGlyThrasnValAlaGlyAsnSerAsnAlaSerAlaTyrIleuAsn 440  
 Db 1317 GTGTACATCATGTCATGACCAATGTCAGCACTCCAAAGCTCGGCTTACCTCAT 1376  
 QY 441 GlySerThrAlaGluLeuAsnThSerAsnTyrSerPhePheThrThrGlyThrGlyGlu 460  
 Db 1377 GTGAGCAGGGCTGACCTTAACCTCCAACTACAGCTTCTTACACCAAGTACAGTGAG 1436  
 QY 461 ThrThrGluIleSerProGluAspThrThrArgIySvIyIySvProValProThrThrSer 480  
 Db 1437 ACCACGAGATCTCCCTGAGAGACAAACGGAAGTACAAAGCTGTTCTTAACCACTCC 1496  
 QY 481 ThrGlyIyGlnProAlaIyThrThrSerThrThrValIleuIleGlnThrThrArgVal 500  
 Db 1497 ACTGGTACCAAGCCGCGATATACCACTCTCAACAGGTGCTCATTCAGACTACCGGTGTG 1556  
 QY 501 ProIySvGlnValAlaValProAlaThraspThrThraspIySvMetGlnThrSerIleuAsp 520  
 Db 1557 CCCAAGCAGGTGGAGTACCCGCGACAGACACACTGACAAAGATGACAAACAGCAGCTGGAT 1616  
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 Db 1617 GAAGCATGAGAGACCAACCAAGTATCATTTGGCTCTTGTGGAGTACTCTGCTACT 1676  
 QY 541 AlaAlaMetLeuIleValPheTyrIleuIleuArgIySvArgHISGlnIleArgSerThrVal 560  
 Db 1677 GCCGCGATGTGATGTCTTCTTAATACTTCGTAAAGCGGACACAGCAGCGAGTACAGTCTC 1736  
 QY 561 ThrAlaAlaArgThrValGluIleIleGlnValAspGluAspIleProAlaAlaThrSer 580  
 Db 1737 ACAGCGCCCGGAGCTGTGAGATATCCAGGTGACGAAGACATCCCGACGAGCAATCC 1796  
 QY 581 AlaAlaAlaThrAlaAlaProSerGlyValSerGlyGluIyAlaValIleuProThr 600  
 Db 1797 GCAGCAGACACAGCAGCTCCGCTCGGTATCAGGTGAGGGGCGAGTGTGCTGCCACA 1856  
 QY 601 ILeHISAspHISAlaAsnTyrAsnThrTyrIySvProAlaHISGlyAlaHISLTPThrGlu 620  
 Db 1857 ATTCTATGACCAATATTAACCTAACACCAACCAACAGCAGATGGGGCCACCTGGACAGA 1916  
 QY 621 AsnSerIleuGlyAsnSerIleuHISProThrValIleThrIleSerGluProTyrIleIle 640  
 Db 1917 AACAGCCCTGGGAACTCTCTGCACCCAAGCAGCAGCACTATCTGAACTTATTAATT 1976  
 QY 641 GlnThrHISThrIyAspIyValGlnIleuThrGlnIle 653  
 Db 1977 CAGACCATACCAAGCAAGGTACAGAACTCAATA 2015

# RESULT 7

US-09-989-727-228  
 Sequence 228, Application US/09989727  
 Patent No. US20020072497A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Deamovets, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kljavin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 TITLE OF INVENTION: Acids Encoding the Same  
 FILE REFERENCE: P2730P1C65  
 CURRENT FILING DATE: 2001-11-19  
 PRIOR APPLICATION NUMBER: 60/049787  
 PRIOR FILING DATE: 1997-06-16  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/065186  
 PRIOR FILING DATE: 1997-11-12  
 PRIOR APPLICATION NUMBER: 60/065311  
 PRIOR FILING DATE: 1997-11-13  
 PRIOR APPLICATION NUMBER: 60/066770  
 PRIOR FILING DATE: 1997-11-24  
 PRIOR APPLICATION NUMBER: 60/075945  
 PRIOR FILING DATE: 1998-02-25  
 PRIOR APPLICATION NUMBER: 60/078910  
 PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: 60/083322  
 PRIOR FILING DATE: 1998-04-28  
 PRIOR APPLICATION NUMBER: 60/084600  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/087106  
 PRIOR FILING DATE: 1998-05-28  
 PRIOR APPLICATION NUMBER: 60/087607  
 PRIOR FILING DATE: 1998-06-02  
 PRIOR APPLICATION NUMBER: 60/087609  
 PRIOR FILING DATE: 1998-06-02  
 PRIOR APPLICATION NUMBER: 60/087759  
 PRIOR FILING DATE: 1998-06-02  
 PRIOR APPLICATION NUMBER: 60/087827  
 PRIOR FILING DATE: 1998-06-03  
 PRIOR APPLICATION NUMBER: 60/088021  
 PRIOR FILING DATE: 1998-06-04  
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 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088026  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088028  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088029  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088030  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088033  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088326  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088167  
 PRIOR FILING DATE: 1998-06-05  
 PRIOR APPLICATION NUMBER: 60/088202  
 PRIOR FILING DATE: 1998-06-05  
 PRIOR APPLICATION NUMBER: 60/088212  
 PRIOR FILING DATE: 1998-06-05  
 PRIOR APPLICATION NUMBER: 60/088217  
 PRIOR FILING DATE: 1998-06-05





QY 101 LeuGIuValLeuGIuLeuGIuValArgSerIleArgGlnIleGIuValAlaIlePheAsn 120  
 Db 357 CTGAGAGCTCTGCACTGGGAGGAACTCCATCCGGAGATTGAGTGGGGCCCTTCAAC 416  
 QY 121 G1yLeuAlaSerLeuSerThrLeuGIuLeuPheAspAntTPLeuThrValIleProSer 140  
 Db 417 GGCCTGGCCAGCTCCACACCTCGAGGCTGTTCGCAACTGGCTGACAGTACCTCTTGC 476  
 QY 141 G1yAlaPheGIuTyrLeuSerIleLeuArgGIuLeuTPLeuArgAsnAspProIleGIu 160  
 Db 477 GGGGCTTTGATTGATCTGCTCAAGCTGCGGAGCTTGGCTTCGCAACACCCCATCCAA 536  
 QY 161 SerIleProSerTyrAlaPheAsnArgValProSerLeuMetArgLeuAspLeuGIu 180  
 Db 537 AGCATCCCTCTTACGCTTCAACGGGAGGCTCCCTCCATGCGCTGAGCTGGGGAG 596  
 QY 181 LeuTyrIleLeuGIuTyrIleSerGIuGIuAlaPheGIuGIuLeuPheAsnLeuTyr 200  
 Db 597 CTCAAGAAAGCTGAGATATATCTCTGAGGAGCTTTGAGGGGCTGTTCAACCTCAAGTAT 656  
 QY 201 LeuAsnLeuGIuMetCysAsnIleIleYAspMetProAsnLeuThrProLeuValGIuLeu 220  
 Db 657 CTGAACCTGGGAGATGCAACATTAAGACATGCCAACTCAACCCCTGGTGGGGCTG 716  
 QY 221 GIuGIuLeuGIuMetSerGIuYAsnIlePheProGIuIleArgProGIuSerPheIleGIu 240  
 Db 717 GAGGAGCTGGAGATGTCAGGGAAACATTCCTGAGATCAAGGCTGCTCTCCATGGC 776  
 QY 241 LeuSerSerLeuLeuYLeuLeuTyrValIleAsnSerGIuValSerIleIleGIuArgAsn 260  
 Db 777 CTGACCTCCCTCAAGAGCTCGGGCTCATGAACCTCAAGGTACGCTTATTGAGGGAGAT 836  
 QY 261 AlaPheAspGIuLeuAlaSerLeuValGIuLeuAsnLeuAlaIleAsnAsnLeuSer 280  
 Db 837 GCTTTGAGCGGCTGCTCACTTGAGAACTCAACTGGCCCAAAATCACTCTCTCT 896  
 QY 281 LeuProIleAspLeuPheThrProLeuArgTyrLeuValGIuLeuIleIleIleAsn 300  
 Db 897 TTGCCCATGACCTTTTACCCGCTGAGGTACCTGGTGGAGTTGCATCTACACCAAC 956  
 QY 301 ProTPAsnCysAspCysAspIleLeuTyrLeuAlaIleTPLeuArgGIuTyrIlePro 320  
 Db 957 CCTTGAACCTGATTGATGACATCTCTGAGGTAGCTGGTGGCTTCGAGAGATATATACC 1016  
 QY 321 ThrAsnSerThrCysCysGIuYArgCysIleIleAsnIlePheMetIleMetArgGIuArgTyrLeu 340  
 Db 1017 ACCAATTCACCTGCTGAGCGGCTGTCACTCCATGCAATGCGAGGCGCTACCTC 1076  
 QY 341 ValGIuValAspGlnAlaSerPheGlnCysSerAlaProPheIleMetAspAlaProArg 360  
 Db 1077 GTGGAGGTGGACCAAGGCTCTTCCAGTGTCTGCCCCCTTCATATGAGACCACTCGA 1136  
 QY 361 AspLeuAsnIleSerGIuGIuYArgMetAlaGIuLeuLeuYArgTyrProPheSer 380  
 Db 1137 GACCTCAACATTTCTGAGGGGTGGATGGAGAACTTAAGTGGAGCTCCCTATGTCC 1196  
 QY 381 SerValIleTPLeuLeuProAsnGIuThrValIleAsnSerIleAlaSerIleIleProArg 400  
 Db 1197 TCCGTAAGTGTCTGCTCCAAATGGAGACAGTGCAGCAGGCTCCCGCCACCAAG 1256  
 QY 401 IleSerValLeuAsnAspGIuThrIleAsnPheSerIleValIleLeuSerAspThrGIu 420  
 Db 1257 ATCTGTCTCTCAAGACGCGACCTTGAACTTTTCCACAGTGTCTCTTACAGACCTGG 1316  
 QY 421 ValTyrThrCysMetGIuThrAsnValAlaGIuAsnSerAsnAlaSerAlaTyrLeuAsn 440  
 Db 1317 GTGTACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1376  
 QY 441 GlySerThrAlaGIuLeuAsnThrSerAsnTyrSerPhePheThrThrGIuThrGIu 460  
 Db 1377 GTGACACGGCTGAGACTTAACCTCAACTCAAGCTTCTTCAACCAAGTAAAGTGGAG 1436

QY 461 ThrThrGIuIleSerProGIuAspThrThrArgIleTyrIleProValProThrThrSer 480  
 Db 1437 ACCACGAGATCTCGCTTGAGACACAAACGGAAGTAAAGCTGTCTTACCAACGCTCC 1496  
 QY 481 ThrGIuTyrGlnProAlaTyrThrThrSerThrThrValIleuIleGlnThrThrArgVal 500  
 Db 1497 ACTGTTACACGCGGATATATACCACTTACCAAGGTGTCTCATTCAGTACCTCCGCTG 1556  
 QY 501 ProYsGIuValAlaValProAlaThrAspThrThrAspIleMetGlnThrSerLeuAsp 520  
 Db 1557 CCACAGAGGTGGAGATACCCCGACAGACACCACTGACAAAGATGACAGACAGCTGGAT 1616  
 QY 521 GluValMetIleThrThrIleIleIleGIuCysPheValAlaValThrLeuLeuAla 540  
 Db 1617 GAAGTCATGAAGACCAACCAAGATCATGCTGCTTGTGGCAGAGCTGTGCTAGCT 1676  
 QY 541 AlaAlaMetLeuIleValIlePheTyrIleLeuArgIleArgIleGlnIleAspSerThrVal 560  
 Db 1677 GCCGCATGTGATTGCTTCTTAACTTCGTAAGGGGACCAAGCAGGAGATACAGTC 1736  
 QY 561 ThrAlaIleArgThrValGIuIleIleGIuValAspGIuAspIleProAlaIleThrSer 580  
 Db 1737 ACAGCCGCGGAGCTGTGAGTATATCCAGTGGACGAAAGCATCCACAGCAACATCC 1796  
 QY 581 AlaAlaIleThrAlaIleProSerGIuValSerGIuGIuValAlaValLeuProThr 600  
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 QY 601 IleIleAspIleIleAsnTyrThrThrTyrIleProAlaIleGIuValIleIleIleIle 620  
 Db 1857 ATTATGACCATATATTAATCTCAACACCTACAAACAGACATGGGGCCACTGGACGAA 1916  
 QY 621 AsnSerLeuGIuAsnSerLeuIleIleProThrValThrThrIleSerGIuProTyrIleIle 640  
 Db 1917 AACAGCTGGGAACTCTGACCCCAAGTACCACTATCTCTGAACCTTATATATT 1976  
 QY 641 GlnThrIleThrIleAspIleValGIuIleThrGlnIle 653  
 Db 1977 CAGACCATACCAAGGATACAGAACTCAATA 2015

RESULT 8  
 US-09-989-731-228  
 ; Sequence 228, Application US/09989731  
 ; Patent No. US20020103125A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Deenoyers, Luc  
 ; APPLICANT: Batson, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary B.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Collin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: P2730P1C70  
 ; CURRENT APPLICATION NUMBER: US/09/989, 731

[illegible]

PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090862  
 PRIOR FILING DATE: 1998-06-26  
 PRIOR APPLICATION NUMBER: 60/090863  
 PRIOR FILING DATE: 1998-06-26  
 PRIOR APPLICATION NUMBER: 60/091360  
 PRIOR FILING DATE: 1998-07-01  
 PRIOR APPLICATION NUMBER: 60/091478  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091544  
 PRIOR FILING DATE: 1998-07-01  
 PRIOR APPLICATION NUMBER: 60/091519  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091626  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091633  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091978  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.: 0 Length: 2185  
 Score: 3407.00 Matches: 648  
 Percent Similarity: 99.39% Conservative: 1  
 Best Local Similarity: 99.23% Mismatches: 4  
 Query Match: 98.87% Indels: 0  
 DB: 10 Gaps: 0

US-09-991-053-10 (1-653) x US-09-989-731-228 (1-2185)

QY 1 MetLysLeuLeuTTPGlnValThyValHisSHSTHTTPASNAAlleLeuLeuPro 20  
 Db 57 ATGAAGCTCTTGCGAGGTAACGTGTGACCAACCACTGGAAGCCATCTGTCCCG 116  
 QY 21 PheValTyrLeuThrAlaGlnValTrpLeuCysAlaIleLeuAlaIleAlaSer 40  
 Db 117 TTGCTTACCTCACGCGCCAGATGTGATTCGTGTGCAAGCCATCTGTGCGCTTCA 176  
 QY 41 AlaGlyProGlnAsnCyseProSerValCysSerCysSerAsnGlnPheSerIleVal 60  
 Db 177 GCCGGGCCCAAGATGCCCCCTCGTTGCTGCTGCAATTAACAGTTCAGCAAGTGTG 236  
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 Db 237 TGCAGCGCCCGGGGCTCTCCGAGGTCCCGCAGGATATTCCTCGAACACCGGTAACCTC 296  
 QY 81 AsnLeuMetGluAsnAsnIleGlnMetIleGlnAlaAspThrPheArgHisLeuHis 100  
 Db 297 AACCTCATGAGAACAAACATCCAGATGATCCAGGCCACACCTTCCGCACTCCACAC 356  
 QY 101 LeuGluValLeuGlnLeuGlyArgAsnSerIleArgGlnIleGluValAlaPheAsn 120  
 Db 357 CTGAGGCTCTGCACTTGGGAGGAACTCCATCCGCAAGATTGAGGTGGGGCTTCAAC 416  
 QY 121 GlyLeuAlaSerLeuSerThrLeuGluLeuPheAspAsnTrpLeuThrValIleProSer 140  
 Db 417 GGCCTGGCCAGCCTCAACACCTCGAGGCTGTTGCAAACTGGCTGACAGTATCCCTTGC 476  
 QY 141 GlyAlaPheGluTyrLeuSerTyrLeuArgGluLeuTrpLeuArgAsnAsnProIleGlu 160  
 Db 477 GGGGCTTGAATACCTGTCAGAGCTGCGGAGCTCTGCTTCGCAACACCCCAATCA 536  
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 Db 537 AGCATCCCTCTTACGCTTCAACCGGGTGCCTCCCTCATATGCGCTGAGCTTGGGGAG 596  
 QY 181 LeuValLeuGluTyrIleSerGluGlyAlaPheGluGlyLeuPheAsnLeuValTyr 200  
 Db 597 CTCAAGAGCTGAGATATCTCTGAGGAGCTTTTGAAGGCGCTTCAACCTCAAGTAT 656

QY 201 LeuAsnLeuGlyMetCysAsnIleLeuAspMetProAsnLeuThrProLeuValGlyLeu 220  
 Db 657 CTBACTTGGGAGATGAGCAACATTTAAAGACATGCCCAATCTCACCCCGGTGGGGCTG 716  
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 Db 777 CTGAGCTCCCTCAAGAGCTCTGAGTCATATACTCACAGGTCAAGCTGATTTGAGCGGAT 836  
 QY 261 AlaPheAspGlyLeuAlaSerLeuValGluLeuAsnLeuAlaHisAsnAsnLeuSerSer 280  
 Db 837 GCTTTGACGGGCTGGCTTCACTTGTGGAATCAACTGGCCCAACAATACTCTCTTCT 896  
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 Db 957 CTTGGAACTGTGATGTGACATTCGTGCTTACCTTGGCTTGCAGATATATACC 1016  
 QY 321 ThrAsnSerThrCysCysGlyArgCysHisAlaProMetHisMetArgGlyArgTyrLeu 340  
 Db 1017 ACCAATTCACCTGCTGTGGCCCGCTGCATGCTCCCATGCAATGGAGGCCGCTACCTC 1076  
 QY 341 ValGluValAspGlnAlaSerPheGlnCysSerAlaProPheIleMetAlaProArg 360  
 Db 1077 GTGAGAGTGAGCAGGCTCTTCCAGTGTGCTGCCCCCTTCAATCAGAGCAAGCACTCGA 1136  
 QY 361 AsnLeuAsnIleSerGluArgMetAlaGluLeuLysCysArgTrpProPheMetSer 380  
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 Db 1257 ATCTGTCTCTCAACGACGCGCACCTTGAACTTTCCACGCTGTGCTTTCAGACACTGG 1316  
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 Db 1437 ACCACGAGATCTCGCTCGAGACACAAACGGAAGTAACAGCTGTCTTCAACCACTCC 1496  
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 Db 1557 CCCAAGCAGGTGGAGTACCGCGACACAGACCACTCAAGATGACAGACAGCTGGAT 1616  
 QY 521 GluValMetLysThrThrLysIleIleGlyCysPheValAlaValThrLeuLeuAla 540  
 Db 1617 GAAGTCATGAAGACCAACCAAGATCATGTGCTTGTGGCAGAGCACTCTCTAGCT 1676  
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 Db 1677 GCCGCATGTTGATGTCTTCTTAATACTTCGTAAAGCGGACCAAGAGGAGTACAGTC 1736

QY 561 ThrAlaAlaArgThrValGluIleIleGlnValAspGluAspIleProAlaAlaThrSer 580  
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RESULT 9  
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Sequence 228, Application US/09989732  
Patent No. US20020123463A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Thomas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2730FIC57  
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 Qy 441 GlySerThrAlaGluAnzAnzThrSerAnzTyrSerPhePheThrThrGlyGlu 460  
 Db 1377 GTGAGCAGCGGTGCTTAAACCTCACTACAGCTTCTTCAACCAAGTAACAGTGGAG 1436  
 Qy 461 ThrThrGluIleSerProGluAspThrThrArgGlySerTyrAspProValProThrThrSer 480  
 Db 1437 ACCACGAGATCTGCTCTGAGACACAAACCGAAAGTCAAGCTGTCTTCTTCAACAGCTCC 1496  
 Qy 481 ThrGlyTyrGlnProAlaTyrThrThrSerThrThrValLeuIleGlnThrThrArgVal 500  
 Db 1497 ACTGTTACAGCGCGGATATACACCTTACACAGGTGCTCATTCAGACTACCGGTGTG 1556  
 Qy 501 ProGlyGlnValAlaValProAlaThrAspThrThrAspTyrMetGlnThrSerLeuAsp 520  
 Db 1557 CCCAAGCAGGTGGAGTACCAGCGACAGACACCACTGACAAAGATGACAGACCGCTGGAT 1616  
 Qy 521 GluValMetLeuThrThrThrValIleIleGlyCysPheValAlaValThrLeuVal 540  
 Db 1617 GAGTTCATGAGAACACCAACAGATCATATGGCTGTGCTTGTGGAGTCACTGTCTAGCT 1676  
 Qy 541 AlaAlaMetLeuIleValPheTyrLeuArgGlyAsnHisGlnGlnArgSerThrVal 560  
 Db 1677 GCGCGCATGTTGATGTCTCTTAATTAACCTGTAAAGGCGACCGACGCGGAGTACAGTC 1736  
 Qy 561 ThrAlaAlaArgThrValGluIleIleGlnValAspGluAspIleProAlaAlaThrSer 580  
 Db 1737 ACAGCCCGCGGACTGTGATATATCAGGTGACCAAGACATCCCGACGCAACATCC 1796  
 Qy 581 AlaAlaAlaThrAlaAlaProSerGlyValSerGlyGluGlyAlaValIleLeuProThr 600  
 Db 1797 GCACAGCAACAGCAAGCTCCGTCGGTGTGATCAGGTAGGGGAGTGTGCTCCCA 1856  
 Qy 601 IleHisAspHisIleAnzTyrAsnThrTyrLeuProAlaHisGlyAlaHisTyrThrGlu 620  
 Db 1857 ATTCAATGACATATTAATTAATCAACACTTACAAACAGACATGGGCGCCACTGACAGAA 1916  
 Qy 621 AnzSerLeuGlyAnzSerLeuHisProThrValThrThrIleSerGluProTyrIleIle 640  
 Db 1917 AACAGCTGGGGAATCTCTGCAACCCACAGTCAACCACTATCTGTGAACCTTATATAT 1976  
 Qy 641 GlnThrHisThrTyrAspTyrValGlnGluThrGlnIle 653  
 Db 1977 CAGACCAATACCAAGACAAAGTACAGAAATCTAAATA 2015

RESULT 11  
 US-09-990-442-228  
 ; Sequence 228, Application us/09990442  
 ; Patent No. US20020132252A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Bostein, David  
 ; APPLICANT: Deenoyere, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Kijavlin, Ivar J.  
 ; APPLICANT: Napier, Mary A.



PRIOR APPLICATION NUMBER: 60/090557  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090676  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090678  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090690  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090694  
 PRIOR FILING DATE: 1998-06-25  
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 PRIOR FILING DATE: 1998-06-25  
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 PRIOR APPLICATION NUMBER: 60/090863  
 PRIOR FILING DATE: 1998-06-26  
 PRIOR APPLICATION NUMBER: 60/091360  
 PRIOR FILING DATE: 1998-07-01  
 PRIOR APPLICATION NUMBER: 60/091478  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091544  
 PRIOR FILING DATE: 1998-07-01  
 PRIOR APPLICATION NUMBER: 60/091519  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091626  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091633  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091978  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.: 0 Length: 2185  
 Score: 3407.00 Matches: 648  
 Percent Similarity: 99.33% Conservative: 1  
 Best Local Similarity: 99.23% Mismatches: 4  
 Query Match: 98.87% Indels: 0  
 DB: 10 Gaps: 0

US-09-991-053-10 (1-653) x US-09-990-442-228 (1-2185)

QY 1 MetLysLeuLeuTrpGlnValThrValHisHisThrTPAanaIleLeuLeuPro 20  
 DB 57 ATGAAGCTCTTGTGGAGTAACGTGCACACACACCTGGAATGCATCTCTCCG 116  
 QY 21 PheValTyrLeuThrAlaGlnValTPrLLeuCySaIaIaIaIaIaIaIaIaIa 40  
 DB 117 TTCCTCAACCTCAGCGGCAAGTGTGATCTGTGTGACAGCATCGTGCCTCA 176  
 QY 41 AlaGlyProGlnAsnCySProSerValCysSerCysSerAsnGlnPheSerValVal 60  
 DB 177 GCCGGGCCCCGAACCTGCCCTCCGTTTGTCTGTGCACTACAGTTCAGGAAGGTGTG 236  
 QY 61 CysThrArgArgGlyLeuSerGlyValProGlnGlyIleProSerAsnThrArgTyrLeu 80  
 DB 237 TGCACGGCGCGGCGCTCTCCGAGGTCCCGCAGGGTATTCCTCGAACACCGGCTACCTC 296  
 QY 81 AsnLeuMetGluAsnAsnIleGlnMetIleGlnAlaAspThrPheArgHisLeuHisHis 100  
 DB 297 AACCTCATGGAGAACATCATCATGATCCAGGCGGACACCTTCGACCTCACACAC 356  
 QY 101 LeuGluValLeuGlnLeuGlyArgAsnSerIleArgGlnIleGlnValAlaPheAsn 120  
 DB 357 CTGAAGGCTCTGCAAGTGTGGCAAGAACTCCATCCGCGAATTGAGTGGGGCTTCAC 416  
 QY 121 GlyLeuAlaSerLeuSerThrLeuGluLeuPheAspAsnThrPLeuThrValIleProSer 140

DB 417 GGCCTGGCAGCTCAACACCTGAGCTGTGACAACTGGCTGACATCATCTCCTAGC 476  
 QY 141 GValAlaPheGluTyrLeuSerLysLeuArgGluLeuThrPLeuArgAsnProIleGlu 160  
 DB 477 GGGGCTTTGAAATACCTGTCACAGCTGGGAGCTGTGGCTTCGCAACACCCCATGAA 536  
 QY 161 SerIleProSerTyrAlaPheAsnArgValProSerLeuMetArgLeuAspLeuGlyIle 180  
 DB 537 AGCATCCCTCTTAACGCTTCAACCGGGTCCCTCCCTCATGCGCTGCACTGGGGAG 596  
 QY 181 LeuLysLysLeuGluTyrIleSerGluValAlaPheGluGlyLeuPheAsnLeuLysTyr 200  
 DB 597 CTCAGAAGCTGGAGTATCTCTGAGGGAGCTTTTGAAGGGCTTCACACTCAAGTAT 656  
 QY 201 LeuAsnLeuGlyMetCysAsnIleLysAspMetProAsnLeuThrProLeuValGlyLeu 220  
 DB 657 CTGAACCTTGGGCAATGCAACATTAAAGACATGCCAATCTCACCCCTGGTGGGCTG 716  
 QY 221 GlnGluLeuGluMetSerGlyAsnHisPheProGluIleArgProGlySerPheHisGly 240  
 DB 717 GAGGAGCTGAGATGTACGGGAACCACTTCCTGAGTCAAGCTGCTCTTCATATGCC 776  
 QY 241 LeuSerSerLeuLysLysLeuTrpValMetAsnSerGlnValSerLeuIleGluArgAsn 260  
 DB 777 CTGAGCTCCCTCAAGAGCTCTGGGTCATGAACCTCAAGCTGACCTGATTGACCGGAAT 836  
 QY 261 AlaPheAspGlyLeuAlaSerLeuValGluLeuAsnLeuAlaHisAsnAsnLeuSerSer 280  
 DB 837 GCTTTTACGGCGGCTTCATCTTGGAACCTCAACTGGCCCAACAATACCTCTCTCT 896  
 QY 281 LeuProHisAspLeuPheThrProLeuArgTyrLeuValGluLeuHisLeuHisAsn 300  
 DB 897 TTGCCCATACCTCTTACCCCGCTAGGTAAGTGTGAGATTCATCAACCAAC 956  
 QY 301 ProTrpAsnCySaPLeuTrpValLeuTrpLeuAlaTrpTrpLeuArgGluTyrIlePro 320  
 DB 957 CCTTGAAGTGTGATGTGACATTTCTGTGCTAGCTGAGCTGTGAGATATATATACCC 1016  
 QY 321 ThrAsnSerThrCysGlyArgGlyHisAlaProMetHisMetAlaGlyArgTyrLeu 340  
 DB 1017 ACCAATTCACCTGCTGTGGCCGCTGTCATGCTCCCATGACATGACAGCGGTACTCC 1076  
 QY 341 ValGluValAspGlnAlaSerPheGlnCysSerAlaProPheIleMetAspAlaProArg 360  
 DB 1077 GTGAGGTGAGACAGGCTCTCTTCCAGTCTTCCCTTCATCATGACACCACTCGA 1136  
 QY 361 AspLeuAsnIleSerGluGlyArgMetAlaGluLeuLysCySaArgThrProProMetSer 380  
 DB 1137 GACCTCAACATTTCTGAGGTCGGATGGCAGAACTTAAGTGTGGACTCCCTCATATGCC 1196  
 QY 381 SerValLysTrpLeuLeuProAsnGlyThrValLeuSerHisAlaSerArgHisProArg 400  
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 QY 401 IleSerValLeuAsnAspGlyThrLeuAsnPheSerHisValLeuLeuSerAspThrGly 420  
 DB 1257 ATCTTGTCTTCAACGAGGACCTTGAACCTTTTCCACGAGTGTCTTTCAGACATGGG 1316  
 QY 421 ValTyrThrCysMetGlyThrAsnValAlaGlyAsnSerAsnAlaSerAlaTyrLeuAsn 440  
 DB 1317 GTGTACACATGACATGATGATCAATGTTGACAGGCACTCAACGCTGGCTTACCTCAT 1376  
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 DB 1377 GTGAGCAGCGCTGACTTAACCTCCACATACAGCTTCTTTCACACAGTAACAGTGGAG 1436  
 QY 461 ThrThrGluIleSerProGluAspThrThrArgLysTyrLysProValProThrThrSer 480  
 DB 1437 ACCACGAGATCTGCTGTGAGACACACCGGAAAGTAAAGCTGTTCTTCAACACCTCC 1496  
 QY 481 ThrGlyTyrGlnProAlaTyrThrThrSerThrThrValLeuIleGlnThrThrArgVal 500  
 DB 1497 ACTGTTAACACGCGGCAATATACACCTTACACAGGTGTGATTCAGATACCGGTGTG 1556



PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
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PRIOR FILING DATE: 1998-06-17  
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PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
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PRIOR FILING DATE: 1998-06-18  
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PRIOR FILING DATE: 1998-07-01

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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.: 0 Length: 2185  
Score: 3407.00 Matches: 648  
Percent Similarity: 99.39% Conservative: 1  
Best Local Similarity: 99.23% Mismatches: 4  
Query Match: 98.87% Indels: 0  
DB: 10 Gaps: 0

US-09-991-053-10 (1-653) X US-09-991-163-228 (1-2185)

QY 1 MeltylsleuLeuTTPGlnValThrValHisHisThrTrpAsnAlaIleLeuLeuPro 20  
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QY 21 PheValTyrLeuThrAlaGlnValTrpIleLeuCysAlaIleAlaIleAlaIleSer 40  
Db 117 TTGCTTACCTCAGCGGCGAAGTGTGATTTCTGTGTCAAGCATTCCTGCGCCCTCA 176  
QY 41 AlaGlyProGlnAsnCyProSerValCysSerCysSerAsnGlnPheSerValVal 60  
Db 177 GCGGGGCCCAAGACTGCGCCCTTCCTGCTGCGTCAAGTAAACAGTCAAGAGTGTG 236  
QY 61 CysThrArgArgGlyLeuSerGlyValProGlnGlyIleProSerAsnThrArgTyrLeu 80  
Db 237 TGCAGCGCGCGGCGCTCTCCGAGGTCCGCGAGGTATTCCTCGAAACCCGCTACCTC 296  
QY 81 AsnLeuMetGluAsnAniIleGlnMetIleGlnAlaSerThrPheArgHisIleuHis 100  
Db 297 AACCTCATGGAACAATCATCATGATGATCCAGGCCCAACCTTCGCACTCCACAC 356  
QY 101 LeuGluValLeuGlnLeuGlyArgAsnSerIleArgGlnIleGluValAlaPheAsn 120  
Db 357 CTGAGAGCTCTGCACTTGGGAGGAGACTCATTCGCGCAGATTGAGTGGGCGCTTCAAC 416  
QY 121 GlyLeuAlaSerLeuSerThrLeuGlnLeuPheAsnThrProLeuThrValIleProSer 140  
Db 417 GGCCTGGCCAGCTCAACACCTGAGCTGTTCGAACAATGGCTGACAGTATCCTTAC 476  
QY 141 GlyAlaPheGlyTyrLeuSerTyrLeuArgGlnLeuThrLeuAspAsnProIleGlu 160  
Db 477 GGGGCTTTGAAATCCTGTCACAGCTGGGAGCTGTGGCTTCGCAACCAACCTCAAA 536  
QY 161 SerIleProSerTyrAlaPheAsnArgValProSerLeuMetCysLeuAspLeuGlyGlu 180  
Db 537 AGCATCCCTCTTACGCTTCAACCGGAGTCCCTCCTCATGCGCTGAGATTGGGGAG 596  
QY 181 LeuIleValLeuGlnTyrIleSerGluGlyAlaPheGlnGlyLeuPheAsnLeuIleTyr 200  
Db 597 CTCAAGAACTGAGGATATCTGTGAGGAGCTTTTGAAGGGCTGTTCACCTCAAGTAT 656  
QY 201 LeuAsnLeuGlyMetCysAsnIleValAspMetProAsnLeuThrProLeuValGlyLeu 220  
Db 657 CTGAACCTGGGCACTGCAACATTAAAGACATGCCAATCCACCCCTGCTGGGCGCTG 716  
QY 221 GluGluLeuGluMetSerGlyAsnHisPheProGluIleArgProGlySerPheHisGly 240

Db 717 GAGGAGCTGGAGATGTCAGGAAACATTCCTCCAGATCAGGCTGGCTCTCCATGAC 776  
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 Db 777 CTGAGCTCCCTCAAGAGCTCTGGGTCATGAATCAAGCTCAGCTGATTAAGGCGAAT 836  
 Qy 261 AlaPheArgGlyLeuAlaSerLeuValGluLeuAsnLeuAlaHisAsnAsnLeuSerSer 280  
 Db 837 GCTTTGACGGGCTGGCTTCACTTGAGAACTCACTTGAGCCCAATTAACCTCTCTCT 896  
 Qy 281 LeuProHisAspLeuPheThrProLeuArgGlyLeuValGluLeuHisLeuHisAsn 300  
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 Db 1017 ACCAATTCACCTGCTGTCGGCGCTGTCACTGCCATGACATGCGAGGCGGCTACCTC 1076  
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 Qy 361 AspLeuAsnIleSerGlyGlyArgMetAlaGluLeuLysCysArgThrProPheMetSer 380  
 Db 1137 GACCTCAACATTTCTGAGGGTGGATGGCAGAACTTAAGTGTGCACTCCCTATGTC 1196  
 Qy 381 SerValLysTrpLeuLeuProAsnGlyThrValLysSerHisAlaSerArgHisProArg 400  
 Db 1197 TCCGAGAGTGGTGTGCTGCCCAATGGAGACAGTGTACAGCAGCGCTCCGCCACCAAG 1256  
 Qy 401 IleSerValLeuAsnAspGlyThrLeuAsnPheSerHisValLeuLeuSerAspThrGly 420  
 Db 1257 AACTGTGCTCAAGACGAGCGACCTTGAACTTTTCCACAGTGTCTCTTCAACACTGG 1316  
 Qy 421 ValTrpThrCysMetGlyThrAsnValAlaGlyAsnSerAsnAlaSerAlaTrpTrpLeuAsn 440  
 Db 1317 GTGTACATGATGATGTGACCAATGTGGAGGCAACTCCAAAGCTTCGGCTCACTTCANT 1376  
 Qy 441 GlySerThrAlaGluLeuAsnThrSerAsnTrpSerPhePheThrThrGlyGlu 460  
 Db 1377 GTGACGAGCGGTGAGCTTAACCTCCCACTACAGTTCTTACCACAGTAACAGTGAG 1436  
 Qy 461 ThrThrGlnIleSerProGluAspThrThrArgGlyGlyTrpLysProValProThrThrSer 480  
 Db 1437 ACCACGGAATCTCGCTGAGACACACAGCAAAAGTACAAAGCTGTCTCTCAACAGTCC 1496  
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 Db 1497 ACTGTACACAGCCGCGCATATACCACTTACCAAGTCTCATTCACAGTACCCGTGTG 1556  
 Qy 501 ProLysGlnValAlaValProAlaThrAspThrThrAspLysMetGlnThrSerLeuAsp 520  
 Db 1557 CCCAAGCAGGTGAGAGTACCCGCGACAGACACACATGAGAAATGAGACGAGCTGAGT 1616  
 Qy 521 GluValMetLysThrThrLysIleIleIleGlyCysPheValAlaValThrLeuLeuAla 540  
 Db 1617 GAAGTCATGAAACCAACCAAGATCATCTGCTGTGGCAGTGTCTGCTAGCT 1676  
 Qy 541 AlaAlaMetLeuIleValPheTrpLysLeuAlaGlyLysArgHisGlnGlnArgSerThrVal 560  
 Db 1677 GCCGCATGTTGATGTTCTTCTAATACTTCGTAAGCCGACACAGAGGGAGTACAGTC 1736  
 Qy 561 ThrAlaAlaArgThrValGluIleIleGlnValAspGluAspIleProAlaAlaThrSer 580  
 Db 1737 ACAGCGCGCGAGCTGTGAGTAATCCAGGTGAGAGAAAGATCCGACAGCAACATATC 1796  
 Qy 581 AlaAlaAlaThrAlaAlaProSerGlyValLysGlyGluGlyAlaValValLeuProThr 600  
 Db 1797 GCAGCAGCAACAGCAGCTCGTCCGCTGTATCAGGTGAGGGGCGAGTATGCTGCCACA 1856

Qy 601 IleHisAsnHisIleAsnTrpAsnThrTrpLysProAlaHisGlyAlaHisTrpThrGlu 620  
 Db 1857 ATTCATGACCATATTAATTACTAACACCTACCAACACAGACATGGGCCCACTGACAGAA 1916  
 Qy 621 AsnSerLeuGlyAsnSerLeuHisProThrValAlaThrThrIleSerGluProTrpIleGly 640  
 Db 1917 AACAGCTGGGGAACCTCTGCAACCCCAAGTCAACACTATCTGTGAACCTTATATTAAT 1976  
 Qy 641 GlnThrHisThrLysAspLysValGlnGluThrGlnIle 653  
 Db 1977 CAGACCATACCAAGACAGAGTACAGGAATCAATA 2015  
 RESULT 13  
 us-09-993-604-228  
 ; Sequence 228, Application US/09993604  
 ; Patent No. US20020137075A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Deans, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerlisen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Kijavlin, Ivar J.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas P.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhong, Zemin  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2730P1C25  
 ; CURRENT APPLICATION NUMBER: US/09/993,604  
 ; CURRENT FILING DATE: 2001-11-14  
 ; PRIOR APPLICATION NUMBER: 60/049787  
 ; PRIOR FILING DATE: 1997-06-16  
 ; PRIOR APPLICATION NUMBER: 60/062250  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/065186  
 ; PRIOR FILING DATE: 1997-11-12  
 ; PRIOR APPLICATION NUMBER: 60/065311  
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 ; PRIOR FILING DATE: 1998-06-02  
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 ; PRIOR FILING DATE: 1998-06-02  
 ; PRIOR APPLICATION NUMBER: 60/087759  
 ; PRIOR FILING DATE: 1998-06-02



Percent Similarity: 99.39%  
 Best Local Similarity: 99.23%  
 Query Match: 98.87%  
 DB: 10  
 Gaps: 0

US-09-991-053-10 (1-653) x US-09-993-604-228 (1-2185)

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 41 AlaGlyProGlnAsnCyProSerValCySerCySerAsnGlnPheSerIYrVal 60  
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 417 GCCCTGGCCAGGCTCAACACCTGAGAGCTGTTCGACAACTGGCTACAGTACTCCCTAGC 476  
 141 GlyAlaPheGluIYrLeuSerIYrLeuArgGluLeuTrpLeuArgAsnProIleGlu 160  
 477 GGGGCTTTGAATACCTGTCCAAGCTGCGGAGCTCTGGCTTCGCAACACCCCATCGAA 536  
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1017 ACCAATTCACCTGCTGTGGCGGCTGTGATGCTCCATGCATGACGAGCGGCTACTC 1076  
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 641 GlnThrHisThrIYrAspIYrValGluGluThrGlnIle 653  
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RESULT 14

US-09-990-456-228

; Sequence 228 Application US/09990456

; Patent No. US20020137890A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.



APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Inc.  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Klavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C22  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

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 Best Local Similarity: 99.23% Mismatches: 4  
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US-09-991-053-10 (1-653) x US-09-990-456-228 (1-2185)

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 Qy 461 ThrThriGluSerProGluAspThrThraGlyTyIysProValProThrThrSer 480  
 Db 1437 ACCACGAGATCTCGCTGAGAGACACACGGAAGTACAGCCTGTTCTTACACAGCTCC 1496  
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RESULT 15  
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 Sequence 228, Application US/09989721  
 Patent No. US20020142961A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
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APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
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 FILE REFERENCE: P2730P1C5  
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Alignment Scores:  
 Pred. No.: 0 Length: 2185  
 Score: 3407.00 Matches: 648  
 Percent Similarity: 99.39% Conservative: 1  
 Best Local Similarity: 99.23% Mismatches: 4  
 Query Match: 98.87% Indels: 0  
 DB: 10 Gaps: 0

US-09-991-053-10 (1-653) x US-09-989-721-228 (1-2185)

QY 1 MetlyseuleutTPGlnValThVaJHshishrTPdamaJalileuleuPro 20  
 DB 57 ATGAAGCTCTTGCGAGGTAACTGTGCACACCACTGGAATGCCATCTGCTCCG 116  
 QY 21 PheValTYrLeuTrrAlaGlnValTrrileuCyValAlaAlaAlaAlaSer 40  
 DB 117 TTGCTTACCTCAGCGGCGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 176  
 QY 41 AlaGlyProGlnAncyProSerValCySerCySerAenglnPheSerIyVal 60  
 DB 177 GCCGGGCCCGAAGTGCCTCCGTTTGTCTGTGTGTGTGTGTGTGTGTGTGTGT 236  
 QY 61 CysThrArgArgGlyLeuSerGluValProGlnGlyIleProSerAenThArgTyleu 80  
 DB 237 TGACGCGCCCGGGGCTCTCCGAGGTCCCGAGGGGTATTCCTGGAACACCCGGTACCTC 296  
 QY 81 AenIeuMetGluAmaAenIleGlnMetIleGlnIleAerThPheArgHisIleu 100  
 DB 297 AACCTCATGAGAACCAATCCAGATGTATCCAGCGCACCTTCCGACCTCCAC 356  
 QY 101 LeuGluValleuGlnLeuGlyArgAenSerIleArgGlnIleGluValAlaPheAen 120  
 DB 357 CTGAGAGCTCTGCACTTGGGAGAACCTCCATCCGCGAGATTGAGTGGGGGCTTCAAC 416  
 QY 121 GlyLeuAlaSerIeuSerThLeuGluIleuPheAenTrrPleuThValIleProSer 140  
 DB 417 GGCCTGCGCACCTCAACACCTGAGCTGTCCAGCAACTGGCTGACAGTATCCCTAGC 476  
 QY 141 GlyAlaPheGluTYrLeuSerIyLeuArgGluIleuTrrPleuAArgAenProIleu 160  
 DB 477 GGGGCTTGTGAATACCTGTCCAGCTGGGAGGCTGGCTTGGCAACACCCATTCGA 536  
 QY 161 SerIleProSerTYrAlaPheAenArgValProSerIeuMetArgLeuAAspLeuGlyGlu 180

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Db 537 AGCATCCCCCTTACGCTTACACCGGGTGCCTCCCTCCATGCGCTGACTGCTGGAG 596
Qy 181 LeuLysLysLeuGluTyrIleSerGluGluValAlaPheGluGluLysPheAsnLeuLysTyr 200
Db 597 CTCAAGAGCTGGAGATATCTCTGAGGAGCTTTTGAGGGCTGTTCACCTCAAGAT 656
Qy 201 LeuAsnLeuGlyMetCysAsnIleLysAspMetProAsnLeuThrProLeuValGlyLeu 220
Db 657 CTGAACCTGGGCATGTGCAACATTAAAGACATGGCCATCTCACCCCTGTGGGGGTG 716
Qy 221 GluGluLeuGluMetSerGlyAsnHisPheProGluIleArgProGlySerPheHisGly 240
Db 717 GAGAGCTGGAGATGTCAAGGAAACCACTCCCTGAGTCAAGCCCTGGCTCTTCATGGC 776
Qy 241 LeuSerSerLeuLysValLeuThrValMetAsnSerGluValSerLeuIleGluAlaArgAsn 260
Db 777 CTGAGCTCCCTCAAGAACCTGTGGGTCAATGAATCTCAAGGTCAAGCTGATTTGAGCGGAT 836
Qy 261 AlaPheAspGlyLeuAlaSerLeuValGluLeuAsnLeuAlaHisAsnAsnLeuSerSer 280
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Qy 281 LeuProHisAspLeuPheThrProLeuArgTyrLeuValGluLeuHisLeuHisAsn 300
Db 897 TTGCCCCATGACCTTTTACCCCGCTGAGTACCTGTGGAGTTGCATCTACACCAAC 956
Qy 301 ProThrPheAspCysAspCysAspIleLeuThrPheLeuAlaThrProLeuArgLysTyrIlePro 320
Db 957 CTTGGAACTGTGATGTGACATTTCTGTGGCTAGCTGTGGCTTGGAGATATATATACC 1016
Qy 321 ThrAsnSerThrCysCysGlyArgCysHisAlaProMetHisMetArgGlyArgTyrLeu 340
Db 1017 ACCAATTCACCTGTGTGTGGCGCTGTATCTCCATGCACATGCGAGCGCTACTCTC 1076
Qy 341 ValGluValAspGlnAlaSerPheGlnCysSerAlaProPheIleMetAspAlaProArg 360
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Qy 361 AspLeuAsnIleSerGluGlyArgMetAlaGluLeuLysCysArgThrProProMetSer 380
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Qy 381 SerValLysTrpLeuLeuProAsnGlyThrValLeuSerHisAlaSerArgHisProArg 400
Db 1197 TCCGGAAGTGTGCTGCTCCCAATGGGACAGTGTCTCAGCCAGCCTCCCGCACCAGAG 1256
Qy 401 IleSerValLeuAsnAspGlyThrLeuAsnPheSerHisValLeuLeuSerAspThrGly 420
Db 1257 ATCTGTGCTCAACAGACGGGACCTTGAACCTTTCCACGTGCTGCTTTCAAGACACTGGG 1316
Qy 421 ValTyrThrCysMetGlyThrAsnValAlaGlyAsnSerAsnAlaSerAlaTyrLeuAsn 440
Db 1317 GTGTACATCATCATGTGTACCAATGTTGACGCACTCCAAAGCTCGGCTACTCACTCAAT 1376
Qy 441 GlySerThrAlaGluLeuAsnThrSerAsnTyrSerPhePheThrThrGlyThrGlyGlu 460
Db 1377 GTGAGCAGCGGTGAGCTTAACCTTCACTCACTCACTTTCACCAAGTAACTGAGAG 1436
Qy 461 ThrThrGluIleSerProGluAspThrThrArgLysTyrLysProValProThrThrSer 480
Db 1437 ACCAGGAGATCTGCTGAGAGACAAAGGAAAGTACAAAGCTGTTCTTACCAAGTGGAG 1496
Qy 481 ThrGlyTyrGlnProAlaTyrThrThrSerThrValLeuIleGlnThrThrArgVal 500
Db 1497 ACTGGTTACCAAGCGGACATATACCACTTCAAGGTGCTCATTCAGACTAACCCGTGTG 1556
Qy 501 ProLysGlnValAlaValProAlaThrAspThrThrAspLysMetGlnThrSerLeuAsp 520
Db 1557 CCCAAGCAGGTGGAGTACCCGCGACAGACCACTGACAGATCAGACCAAGCTTGAT 1616
Qy 521 GluValMetLysThrThrLysIleIleIleGlyCysPheValAlaValThrLeuLeuAla 540

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Db 1617 GAAGTCATGAAGACCAACCAATCATTCATGGCTGCTTTGTGGCAGTGAAGTGTGACT 1676
Qy 541 AlaAlaMetLeuIleValPheTyrLysLeuArgLysArgHisGlnGlnIleArgSerThrVal 560
Db 1677 GCCGCCATGTGATTTGCTTCTTATTAACCTTGTGAAGCGGACCAAGCGGAGTACAGTC 1736
Qy 561 ThrAlaAlaArgThrValGluIleIleGlnValAspGluAspIleProAlaAlaThrSer 580
Db 1737 ACAGCCCGCGAGCTGTTGAGATATCCAGGTGAGCAAGACATCCAGCAGCAACATCC 1796
Qy 581 AlaAlaAlaThrAlaAlaProSerGlyValSerGlyGluGluValAlaValLeuProThr 600
Db 1797 GCGACCAACAACAGCAGCTCCGTCCGTGTATCAGGTGAGGGGCGAGTAGTGTGCCACA 1856
Qy 601 IleHisAspHisIleAsnTyrAsnThrTyrLysProAlaHisGlyAlaHisSTPThrGlu 620
Db 1857 ATTATATACCAATTTAATTAATCAACACCTTACAAACCAAGCAGATGGGGCCACTGACAGA 1916
Qy 621 AsnSerLeuGlyAsnSerLeuHisProThrValThrThrIleSerGluProTyrIleIle 640
Db 1917 AACAGCTGGGGAACTCTTGACACCCCAAGTACCACTATCTCTGAACCTTATATATAT 1976
Qy 641 GlnThrHisThrLysAspLysValGlnGluThrGlnIle 653
Db 1977 CAGACCATTAACAAGGACAAAGGTACAGAAACTCAATA 2015

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Search completed: January 23, 2004, 03:29:02  
 Job time : 622 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 22, 2004, 22:07:21 ; Search time 3592 Seconds  
(without alignments)  
4418.381 Million cell updates/sec

Title: US-09-991-053-10  
Perfect score: 3446  
Sequence: 1 MRLMQLVTVHHTWNAILLP.....ISEPIYIOTHTKQKQETQI 653

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues  
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame\_plus\_p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO.spool/US0991053/runat\_22012004\_141113\_17735/app.query.fasta\_1.839  
-DB=EST-QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdt -List=45  
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pct -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US0991053.@CGN\_1\_1.2810@runat\_22012004\_141113\_17735 -NCPU=6 -ICPU=3  
-NO\_MAP -LANG=QUERY -NEG SCORES=0 -WAIT -DSPELACK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
EST: \*  
1: em\_estba: \*  
2: em\_esthum: \*  
3: em\_estin: \*  
4: em\_estmu: \*  
5: em\_estov: \*  
6: em\_estpl: \*  
7: em\_estro: \*  
8: em\_hic: \*  
9: gb\_est1: \*  
10: gb\_est2: \*  
11: gb\_hic: \*  
12: gb\_est3: \*  
13: gb\_est4: \*  
14: gb\_est5: \*  
15: em\_estfun: \*  
16: em\_estom: \*  
17: em\_ges\_hum: \*  
18: em\_ges\_inv: \*  
19: em\_ges\_pin: \*  
20: em\_ges\_vrt: \*  
21: em\_ges\_fun: \*  
22: em\_ges\_mam: \*  
23: em\_ges\_mus: \*  
24: em\_ges\_pro: \*  
25: em\_ges\_rod: \*  
26: em\_ges\_png: \*  
27: em\_ges\_vrl: \*  
28: gb\_ges1: \*

29: gb\_ges2: \*  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3306.5	96.0	2271	11 BC012209	BC012209 Mus muscu
2	2187	63.5	2833	11 AK046781	AK046781 Mus muscu
3	1836	53.3	3494	11 AK032467	AK032467 Mus muscu
4	1835	53.3	3097	11 AK034276	AK034276 Mus muscu
5	1835	53.3	3133	11 AK048322	AK048322 Mus muscu
6	1827	53.0	2873	11 AK032088	AK032088 Mus muscu
7	1805.5	52.4	1845	11 BC053486	BC053486 Mus muscu
8	1794.5	52.1	1914	11 BC032460	BC032460 Homo sapi
9	1261	36.6	806	9 AV709803	AV709803 Homo sapi
10	1169	33.9	1303	11 BC019687	BC019687 Homo sapi
11	1108.5	32.2	913	13 BX460831	BX460831 BX460831
12	1067.5	31.0	845	13 BU706148	BU706148 BU706148
13	1043	30.3	803	12 BI916800	BI916800 603177924
14	1037	30.1	870	14 CA978880	CA978880 AGENCOURT
15	1016	29.5	593	14 CA890729	CA890729 B0161B05
16	1002.5	29.1	609	13 BQ340625	BQ340625 PMO-NN025
17	1002	29.1	611	10 BE859884	BE859884 UI-M-A01-
18	988.5	28.7	924	13 BX440523	BX440523 BX440523
19	986.5	28.6	793	14 CA315186	CA315186 UI-M-FW0-
20	981	28.5	946	12 BI522468	BI522468 603175417
21	963	27.9	899	29 CNS0248C	AL180453 Tetradon
22	961.5	27.9	771	29 BX210601	BX210601 Dario rer
23	940	27.3	710	13 BQ178757	BQ178757 UI-M-EV0-
24	932	27.0	883	10 BF165865	BF165865 601774896
25	925	26.8	780	14 CA310827	CA310827 UI-CF-FN0
26	922.5	26.8	752	14 CA749990	CA749990 UI-M-FD0-
27	897.5	26.0	813	13 BQ442328	BQ442328 UI-M-EV0-
28	880	25.5	556	12 BM071178	BM071178 fv03g10.x
29	868	25.2	711	12 BM975435	BM975435 UI-CF-EN1
30	864	25.1	926	29 CENS02YPA	AL219943 Tetradon
31	863.5	25.1	928	10 BQ337189	BQ337189 602434283
32	857	24.9	650	12 BI563160	BI563160 fv89c06.y
33	828	24.0	1100	29 CENS05S08	AL352169 Tetradon
34	825	23.9	556	12 B1706075	B1706075 fg01a05.y
35	798.5	23.0	968	29 CENS03QY6	AL256551 Tetradon
36	792	23.0	470	12 BM964085	BM964085 UI-M-EQ0-
37	790	22.9	580	12 BM070860	BM070860 fv01d04.y
38	784.5	22.8	751	13 BU052969	BU052969 UI-M-FC0-
39	768	22.3	569	12 BM070808	BM070808 fv99f04.y
40	766	22.2	572	10 BG688425	BG688425 336041.BA
41	763	22.1	881	12 B1736237	B1736237 603359928
42	762	22.1	664	13 BQ185392	BQ185392 UI-E-EJ1-
43	755	21.9	540	13 BQ189063	BQ189063 UI-E-EJ1-
44	754	21.9	487	29 BZ239666	BZ239666 CH230-272
45	754	21.9	1134	12 BM928412	BM928412 AGENCOURT

## ALIGNMENTS

RESULT 1  
LOCUS BC012209 2271 bp mRNA  
DEFINITION Mus musculus, clone IMAGE:3995758, mRNA.  
ACCESSION BC012209  
VERSION BC012209.1 GI:15126555  
KEYWORDS HTC.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 2271)  
Straussberg, R.

## TITLE

Direct Submission  
Submitted (06-AUG-2001) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Offices, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,  
USA

## REMARK

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)

Tissue procurement: Gilbert Smith, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome  
Sequencing Center

Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
Gunnarathne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,  
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,  
Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>

Series: IRAX Plate: 23 Row: n Column: 10  
This clone was selected for full length sequencing because it  
passed the following selection criteria: Hexamer frequency ORF  
analysis, Genomescan gene prediction

This clone has the following problem: frame shifted.

## FEATURES

## Source

Location/Qualifiers

1..2271

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="IMAG:3995758"

/tissue\_type="mammary tumor metastasized to lung. Tumor  
arose spontaneously from a senescent normal mammary  
(clonal) outgrowth infected with the virus MMTV."

/clone\_idb="NCI CGAP\_Lu29"

/lab\_host="DH10B"

/note="Vector: pCMV-Sport6"

BASE COUNT 578 a 659 c 522 g 512 t  
ORIGIN

## Alignment Scores:

Prod. No.: 0 Length: 2271  
Score: 3306.50 Matches: 633  
Percent Similarity: 97.71% Conservative: 6  
Best Local Similarity: 96.79% Mismatches: 13  
Query Match: 95.95% Indels: 2  
DB: 11 Gaps: 1

US-09-991-053-10 (1-653) x BC012209 (1-2271)

QY 1 MetlyleuleuLeuTrpGlnValThrValHisHisThrTrpAsnAlaLeuLeuPro 20  
DB 134 ATGAGAGCTCTTGGGAGTAACTGTG---CACACACCTGGAATGCCGTCCTGCC 190  
QY 21 PheValTyrLeuThrAlaGlnValTyrIleLeuCyAlaAlaIleAlaAlaSer 40  
DB 191 GTCGTCACTCAACGGGCAAGTGTGATCTGTGTGACACCAATCGCTGCGCGCTTCA 250  
QY 41 AlAGlyProGlnAnCyProSerValCySerCySerAnGlnPheSerIleValVal 60  
DB 251 GCCGGGCCCCAAGACCTCCCTCGTCTGTCTGCGAACAACATTCACACAGGAGTG 310  
QY 61 CysThrArgArgIleuSerGluValProGlnGlyIleProSerAnThrArgTyrLeu 80  
DB 311 TGACCCGCGGGGAGCTCTGAGGTCCACAGGATTCCTTCAACACCCGATATCTC 370  
QY 81 AsnLeuMetGluAsnAnIleGlnMetIleGlnAlaAspThrPheArgHisIleHis 100  
DB 371 AACCTCATGAAAAACAATCATCATGATTCAGGCCGACACCTTCAGGACCTTCATCAC 430

QY 101 LeuGluValLeuGluLeuGluYarGAnSerIleArgGlnIleGluValAlaPheAsn 120  
DB 431 CTGGAGAGCTCTCAGAGTGGGAGGAACTCCATCAGGACATGAGGTGGGCGCTTCAT 490  
QY 121 GlyLeuAlaSerLeuSerThrIleuGluLeuPheAsnThrIleuThrValIleProSer 140  
DB 491 GGCCTCGCAGCTCAACACCTCGAAGCTGTGACAACTGCTGACATCATCCCACT 550  
QY 141 GlyAlaPheGluTyrLeuSerIleuArgGluLeuTyrIleuArgAsnAnProIleGlu 160  
DB 551 GGGGCTTTGATGACTGCTGCAAACTCGGGAGCTCTGCTGCAAACTCCATTGAG 610  
QY 161 SerIleProSerTyrAlaPheAsnArgValProSerLeuMetArgLeuAspLeuGlyGlu 180  
DB 611 AGATCCCTTCTTATAGCTTCAACCGGGGCTCCCTCATCGTGTGACTTGGGGGAA 670  
QY 181 LeuValYLeuLeuGluTyrIleSerGluGlyAlaPheGluGlyLeuPheAsnLeuYr 200  
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QY 201 LeuAsnLeuGluMetCyAsnIleLeuAspMetProAsnLeuThrProLeuValGlyLeu 220  
DB 731 CTGAAGCTGGGATGTGCAACATTAAGATATGCCAATCTTACACCTGTTGGGCTTC 790  
QY 221 GluGluLeuGluMetSerGlyAsnHisPheProGluIleArgProGlySerPheHisGly 240  
DB 791 GAGGAGCTTGAATGTACAGGAACCACTTCTGAGATCAGGCGTGGCTTCCATGAGC 850  
QY 241 LeuSerSerLeuYLeuYLeuTyrValMetAsnSerGlnValSerLeuIleGluArgAs 260  
DB 851 CTAAAGCTCCCTCAAAAAAATCTGGGTGTGAACTCAACAGCTGATATGAGGGGAA 910  
QY 260 AlaPheAspGlyLeuAlaSerLeuValGluLeuAsnLeuAlaHisAsnAsnLeuSerSe 280  
DB 911 TGTCTTGGAGGAGCTGGCTTCCCTGTGAGACTCAATTAAGCCACAAATACCTTCATC 970  
QY 280 rLeuProHisAspLeuPheThrProLeuArgTyrLeuValGluLeuHisLeuHisAs 300  
DB 971 TTTGGCCCATGACCTTTCACACCCCTGAGATACCTGGTGGATTCATACACCAACA 1030  
QY 300 nProTrpAnCyAspCyAspIleLeuTyrLeuAlaTyrTrpLeuArgGluTyrIle 320  
DB 1031 TCTTGGAACTGTGATGTGATATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1090  
QY 320 oThrAnSerThrCyCyAsGlyArgCyHisIleAlaProMetHisMetArgGlyArgTyrLe 340  
DB 1091 AACCAATTCACCTGCTGTGGCGGCTGTATGCTCCATGACATGCGAGGCGGCTTACCT 1150  
QY 340 uValGluValAspGlnAlaSerPheGlnCySerAlaProPheIleMetAspAlaProAr 360  
DB 1151 GGTAGAGTGGACACAGGCTGCTTTCAGTGTCTGCTGCTTTCATCATGATGACCCGG 1210  
QY 360 gAspLeuAnIleSerGluGlyArgMetAlaGluLeuYCyAsGlyThrProPrometSe 380  
DB 1211 GGAACCTCATATCTCGAGATCGAGTGCAGCAAACTGAATGCGGACCTCCCTATGTC 1270  
QY 380 rSerValYrTrpLeuLeuProAsnGlyThrValLeuSerHisAlaSerArgHisProAr 400  
DB 1271 CTCTGGAAGTGTGTCTCCCAATGGACAGTGTCCACACGCTCCCGGATCCCGG 1330  
QY 400 gIleSerValLeuAsnAspGlyThrLeuAnPheSerHisValLeuLeuSerAspThrG 420  
DB 1331 GATCTCTGTTCCAAAGATGAGCACTTGAACCTTCTCGTGTGCTCATAGACACTGG 1390  
QY 420 yValYrThrCyMetGlyThrAsnValAlaGlyAsnSerAsnAlaSerAlaTyrLeuAs 440  
DB 1391 AGATACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1450  
QY 440 nGlySerThrAlaGluLeuAnThrSerAnThrSerAnThrPhePheThrGlyThrGly 460  
DB 1451 TGTGAGCTGGGCGGAGCTCAACACCCCACTTCACTTCCACCACTGATCACTGATGA 1510  
QY 460 uThrThrGluIleSerProGluAspThrThrArgYrTyrYsProValProThrThrSe 480



DB 1511 AACCCAGAGATATACCTGAGACATACAGGAGATACAGCCTGTTCCACACATC 1570  
 QY rThg1yTyrGlnProAlaIyThrThrSerThrThrValLeuIleGlnThrThrArgVa 500  
 DB 1571 CACTGGTATACAGCGGCGGATATACCACTTACAGAGGTGCTCATTCAGACCACTGGT 1630  
 QY 500 IProlyGlnValAlaValProAlaThrAspThrThrAspLysMetGlnThrSerLeuAs 520  
 DB 1611 GCCCAAGACAGGTGCAGATACCTCCACAGATACCACTGACAGATGACAGACAGCTGGA 1690  
 QY 520 pGluValIeclyThrThrThrLysIleIleIleGlyCysPheValAlaValThrLeuLeu 540  
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 QY 540 aAlaIaIeMetLeuIleValPheTyrLysLeuArgLysArgHisGlnGlnArgSerThrVa 560  
 DB 1751 TGCTCCAGATGATGATGCTTCTTATTAACCTTGCAAGCGGACAGCGGAGTACAGT 1810  
 QY 560 IThzAlaAlaArgThrValGluIleIleGlnValAspGluAspIleProAlaAlaThrSe 580  
 DB 1811 CACAGCTGCAGGACAGATGAGATATATCAGGTGATGAGACATCCACAGCAGCAGCACC 1870  
 QY 580 rAlaAlaAlaThrAlaAlaAlaProSerGlyValSerGlyGluGlyAlaValValLeuProth 600  
 DB 1871 TGCACACACACAGACAGCTCCCTCCGGTGTATCAGGTGAGGGGCGAGTGTGCTCCAC 1930  
 QY 600 rIleHisAspHisIleAsnTyrAsnThrTyrLysProAlaHisGlyAlaHisTyrThrGl 620  
 DB 1931 AATATATGACCATATTAATTAATTAACCACTTACCAACACAGACATGAGGCGCCACTGACAGA 1990  
 QY 620 uAsnSerLeuGlyAsnSerLeuHisProThrValThrThrIleSerGluProTyrIleI 640  
 DB 1991 AAACAGCCTCGGGGAATCTCTCTGACCCCAACACTCACTGAACTTATATAT 2050  
 QY 640 eGlnThrHisThrLysAspLysValGlnGlnThrGlnIle 653  
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RESULT 2  
 LOCUS AK046781 2833 bp mRNA linear HTC 05-DEC-2002  
 DEFINITION Mus musculus 10 days neonate medulla oblongata cDNA, RIKEN full-length enriched library, clone:BB30005D03 product:LIBB-LIKE PROTEIN (FRAGMENT) homolog [Mus musculus], full insert sequence.  
 ACCESSION AK046781.1 GI:26338356  
 VERSION AK046781.1  
 KEYWORDS HTC; CAP trapper.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 AUTHORS Carninci, P. and Hayashiaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636

REFERENCE  
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159

REFERENCE  
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,

Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multiplexillary sequencer  
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861

REFERENCE  
 AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fiedischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nakado, I., Pesole, G., Quackenbush, J., Schriml, L. M., Strubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Baren, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyo-oka, K., Wang, K. H., Weltz, C., Whitaker, C., Wilmberg, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohlschki, S. and Hayashizaki, Y.  
 Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409 (6821), 685-690 (2001)  
 MEDLINE 21085660  
 PUBMED 11217851

REFERENCE  
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
 TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 JOURNAL Nature 420, 563-573 (2002)  
 MEDLINE 12127851

REFERENCE  
 AUTHORS Adachi, J., Aizawa, K., Akimura, T., Aizawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 TITLE Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
 COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.go.jp/  
 URL: http://fantom.gsc.riken.go.jp/  
 URL: http://fantom.gsc.riken.go.jp/  
 Location/Qualifiers  
 1. 2833  
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## CDS

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SAELNPNFSPTTYVETETISPDITKXKVPPTISGCPAATYTSVLIQTRV  
PKQVVPSTIDTDKQTSIDBVKTKTIIIGCFVATLLAAMLIYFYKLRKHQORS  
TYTAATVEIIOVDEDI PAAPAPAAATGAAGVAVLFTIHDHINNTYKPAHGA  
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BASE COUNT 791 a 649 c 685 g 708 t

## ALIGNMENT SCORES:

Pred. No.: 2,36e-214 Length: 2833  
Score: 2187.00 Matches: 416  
Percent Similarity: 97.22% Conservative: 4  
Best Local Similarity: 96.30% Mismatches: 12  
Query Match: 63.46% Indels: 0  
DB: 11 Gaps: 0

US-09-991-053-10 (1-653) x AK046781 (1-2833)

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DB 1 GAGCTGAGATGTCAGGGAACCACTTCCGAGATCGGCTGGCTTCCATGAGCCCTA 60  
QY 242 SERSERIEULYSLYSEUTRVALMETASNSERGLNVALSERLEULIEGLARGAENALA 261  
DB 61 AGCTCCCTCAAAAACGTGGGTGATGATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 120  
QY 262 PHEAPGLYUULASERLEUVALGULLEUENLEULAHISANBANLEUSERSERLEU 281  
DB 121 TTGAGCGAGCTGGCTTCCCTCGTGGAATCACTTGAAGCCCAATTAACCTCTCATCTTTG 180  
QY 282 PROHISASPLEUHERHPRULEUARGYLYLEUVALGULLEUHSIEUHSISASPRO 301  
DB 181 CCCCATGACCTCTTCAACCCCTGAAGTACCTGGTGAAGTGAACCTCAACCAATCCCT 240  
QY 302 TRPASNCSAPCYSAAPLIELEUTRPLEUALATRTPLLEUARGGLUTYRIIEPROTHR 321  
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QY 322 AENSERTHCYSGGLYARGCYSHISALAPROMETHISMETARGGLYARGYLYLEUVAL 341  
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QY 342 GIUVALASPLINLASERPHIEGICYSSERIALAPROPHIELEMETASPLAPROAGAP 361  
DB 361 GAGGTGACACGAGCTGCTTCAAGTGTCTGCCCTTTCATCATGATGACACCCCGGAGAC 420  
QY 362 LEUENALIESERLUGLYARGMETALAGLLEUUYCYARGTHPRPROMETSESER 381  
DB 421 CTCGAATCTCTAGAGATCGGATGCGAAGCTGAAGTGTGGACCTCCCTATATGTACT 480  
QY 382 VALLEYTRPLEUENPROAENGILYTHRVALLEUSERHISLASERARGHISPROARGILE 401  
DB 481 GTGAAGTGTGCTGCGCAATGGAGACAGTCTCAGCACCGCTCCGCGCATCCCGGATC 540  
QY 402 SERVALLEUASNSAPGLYTHIRLEUENPHESERHISVALLEULEUSERAPTHRGYVAL 421  
DB 541 TCTGTTCTCATATATGACACCTTTCCTGCTGTGCTCATGACACTGAGATGA 600  
QY 422 TYRTHCYMEGGLYTHIRAEVALALAGLYASNSERASNLASERIALATYRIEANGILY 441

DB 601 TACACATGATGATGATGACCAATGTCGACAGCAACTCCAAATGCTCCGCGCTACTCATGTG 660  
QY 442 SERTHRAIAGLLEUASNTHERSERANTYRSERPHIEPHEHTRTHGILYGLIYU 461  
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QY 462 THRGULIESERPROGLIUSPHTHRAIGLYLYSPROVALPROTHRTHSERTHR 481  
DB 721 ACAGAGATATCACCTGAGAGACATAACAGGAAGTCAAGCCGTTCACCAATCCACT 780  
QY 482 GLYTRGIPROALATYRTHRTHSERTHRVALLEULEGINTHRTHARGYVALPRO 501  
DB 781 GGTTCACGCGCGGATATACCACTTCAACAGGCTCATTCACAGCCCGCTGTGCC 840  
QY 502 IYSGINVALALAVAPROALATHRAPHTHRAAPLYSMETGLNTHSERLEUENAPGI 521  
DB 841 AAGCAGGTGCGGATGACCTCCACAGATACCACTGACCAAGATGACACCGCTGATGA 900  
QY 522 VALMETEYTHRTHLYGILEILEIEGLCYSPHEVALALAVALTHRLEUENALALA 541  
DB 901 GTCATGAAGACCAACCAATCATCTTGGCTGCTTGTGGAGTACTCTCTACTGCT 960  
QY 542 ALAMETLEULEVALPHELYLYLEUARGLYSARGHISGLINGINARGSERTHRYALTHR 561  
DB 961 GCCATGTGATGCTCTTCTATTAACCTGCAAGCGGACAGCAGCGGAGTACAGTACA 1020  
QY 562 ALAALAAAGTHVALGILIEILEINVALAPGLIUSAPRIIEPROALALATHESEZALA 581  
DB 1021 GCTGCAGACAGTGAAGATTAATCCAGGTGATGAAGACATCCAGCAGCAGCAGCTGCC 1080  
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DB 1081 GCAGCAACGACGCTCCGCTCGGTATACAGTGAAGGCGAGTGTGCTCCCAATA 1140  
QY 602 HISAPHSILIEASNTYASNTHTYRYSAPROALAHISGLYALHISERTHRLGUEN 621  
DB 1141 CATGACATATTAATACAAACACTTAAACACAGACATGGGCGCCACATGACAAATAAC 1200  
QY 622 SERLEUGLYAENSERLEUHSIPROTHRVALTHRTTHRIIESERGLNPROTYRIIELEGIN 641  
DB 1201 ACCCTGGGAGACTCTCTGTGACCCCAAGCAGCAGCAGTATCTTGAACTTAATTAATTCG 1260  
QY 642 THRIESTHLYASPLYEVALGINTHRLGINTILE 653  
DB 1261 ACCCATACCAAGACAGATGACGAAGTCAATAA 1296

RESULT 3  
AK032467  
LOCUS  
DEFINITION  
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ENRICHED LIBRARY, CLONE:6430556C10 PRODUCT:WEAKLY SIMILAR TO BRAIN  
TUMOR ASSOCIATED PROTEIN NMG14 [Homo sapiens], full insert  
sequence.  
ACCESSION  
AK032467  
VERSION  
AK032467.1 GI:26328286  
KEYWORDS  
HTC; CAP trapper.  
SOURCE  
MUS MUSCULUS (HOUSE MOUSE)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 Carrinci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
JOURNAL  
MEDLINE  
99279253  
PUBMED  
10349636  
AUTHORS  
Carrinci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL  
Genome Res. 10 (10), 1617-1630 (2000)

[illegible]

URL: <http://fantom.gsc.riken.go.jp/>.

Location/Qualifiers

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/sex="male"

/tissue\_type="olfactory brain"

/clone\_lib="RIKEN full-length enriched mouse cDNA library"

/dev\_stage="adult"

859. .2781

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polyA\_signal

polyA\_site

BASE COUNT 1055 a 763 c 692 g 984 t

ORIGIN

Alignment Scores:

Pred. No.: 6.32e-178 Length: 3494

Score: 1836.00 Matches: 362

Percent Similarity: 72.40% Conservative: 105

Best Local Similarity: 56.12% Mismatches: 138

Query Match: 53.28% Indels: 41

DB: 11 Gaps: 14

US-09-991-053-10 (1-653) x AK032467 (1-3494)

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Qy 121 GIyIeuAlaSerIleuSerThrIeuGInIleuPhaSpaenTrpIeuThValIleProSer 140

Db 1222 GGTCTGGCAACTTCAACCTCGAGATCTTTTGCAATCGCTTTACATCAATACCGAAT 1281

QY 141 GlyAlaPheGluTyrLeuSerLeuArgGluLeuTyrLeuArgAsnProIleGlu 160  
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 DB 1342 AGCATCCCTTCTTAATGCTTAACAGATCCCTTTGGCGCGCTGAGCTTAAGGGA 1401  
 QY 181 LeuLeuLeuLeuGluTyrIleSerGluGlyAlaPheGluGlyLeuPheAsnLeuTyr 200  
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 QY 281 LeuProHisPheLeuPheThrProLeuArgTyrLeuValGluLeuHisLeuHisAsn 300  
 DB 1702 TTGCTCATGACCTTCACACCTTCGATCTAGAGAGATACACCTTCATCAAC 1761  
 QY 301 ProTyrAsnCysAspCysAspIleLeuTyrLeuAlaTyrTyrLeuArgGluTyrIlePro 320  
 DB 1762 CCGTGAACTGTAACGTGATATCCGTGTGCTCAGCTGGATGAAGACATGGCCCC 1821  
 QY 321 ThrAsnSerThrCysGlyArgCysHisAlaProMetHisMetArgGlyArgTyrLeu 340  
 DB 1822 TCACACACACTGCTGCTGCAAGGTGTAACATCCCCCACTGAAAGGAGATCATC 1881  
 QY 341 ValGluValAspGlnAlaSerPheGlnCysSerAlaProPheIleMetAspAlaProArg 360  
 DB 1882 GGAAGAGCTGACGAGATTAACCTTAACATGCTATGCTCCGTAATGGAGCCCTGCA 1941  
 QY 361 AspLeuAsnIleSerGluGlyArgMetAlaGluLeuLeuLeuCysArg--ThrProMet 379  
 DB 1942 GACCTCAATGCTACGTAAGGATGCGAGCTGAGCTGAATGTGGGCTTCTTACGTCCTG 2001  
 QY 380 SerSerValLeuTyrLeuLeuProAsnGlyThrValLeuSerHisAlaSerArgHisPro 399  
 DB 2002 ACTTCCTGATCTTGATTAACCTCAATGAAAGATCATGACCCAGGGGCAATCAAAAGT 2061  
 QY 400 ArgIleSerValLeuAsnAspGlyThrLeuAsnPheSerHisValLeuLeuSerAspThr 419  
 DB 2062 CGGATACCTGCTGCTCAGCAGCGGATCTTAATTTCAATGTAATGTAAGCAAGACACA 2121  
 QY 420 GlyValTyrThrCysMetGlyThrAsnValAlaGlyAsnSerAsnAlaSerAlaTyrLeu 439  
 DB 2122 GGAGTGAACATGATGAGTAATCTGTTGGCAACCACTGCTTTCGCACCTTG 2181  
 QY 440 AsnGlySerThrAlaGluLeuAsnThrSerAsnTyrSerPhePheThrArgTyrGly 459  
 DB 2182 AATGTTACTGGGCA-----ACCACTACTCCGTTCTCGTACTTTTCAACTGTAACGTA 2235  
 QY 460 GluThrThrGluLeuSerProGluAsp-----ThrThrArgGlyTyrLeuProVal 476  
 DB 2236 GAGACTATGGAACCTTCTCAGATGAGGACACGACACAGATTAACATGAGGCCCACT 2295  
 QY 477 Pro-----ThrThrSerThrGlyTyrGlnProAlaTyrThrThrSerThr 491  
 DB 2296 CCAAGTGAATGATGGAGACCAACCAATGTA-----ACCACATCTCTT 2337

QY 492 ThrValLeuIleGlnThrThrArg---ValProGlyGlnValAlaValProAlaThrAsp 510  
 DB 2338 AGGCCA-----CAGAGCAACAGGTGCAAGAAAAAATTCACCATCCAGTAACTGAC 2391  
 QY 511 ThrThrAspLeuMetGlnThrSerLeuAspGluValMetLeuTyrThrIleIleIle 530  
 DB 2392 ATCAACACAGCGGATC---CCAGGAATTGATGAGGTCAAGAAAAACATTAATCTTAT 2448  
 QY 531 GlyCysPheValAlaValThrLeuLeuAlaAlaMetLeuIleValPheTyrTyrLeu 550  
 DB 2449 GGGTGTGTTTGCGCATCACTCACTGAGCTGCGGATGATGCTGATTTTCTCAAGATG 2508  
 QY 551 ArgTyrArgHisGlnGlnArgSerThrValThrAlaAlaArgThrValGluIleGln 570  
 DB 2509 AGGAACAGACCATCGGCAAAACACCATGCTCCACAGAGAGCTTGAAATCATTAAC 2568  
 QY 571 ValAspGluAspIleProAlaAlaThrSerAlaAlaIleThrAlaAlaProSerGlyVal 590  
 DB 2569 GTGATGATGATGATCACTGGGACACGCCGTG----- 2601  
 QY 591 SerGlyGluGlyAlaValAlaLeuProThrIle---HisAspHisIleAsn---TyrAsn 608  
 DB 2602 -----GAAAGCCACTGCCCATGCTCGATGAGATGACATGACCTTAACCATTAAC 2655  
 QY 609 ThrTyrLeuProAlaHisGlyAlaHisTyrThrGluAsnSerLeuGlyAsnSerLeuHis 628  
 DB 2656 TCTTAACAAATCCCTTCACACACACACAAACAGTAACACAAATA---AATCAATACAC 2712  
 QY 629 ProThrValThrThrIleSerGluProTyrIleIleGlnThrHisThrLeuAspTyrVal 648  
 DB 2713 -----AGTTCAGTGTGATGAACCGTTATGATCGAATGAACTTAAGACAAATGA 2763  
 QY 649 GlnGluThrGlnIle 653  
 DB 2764 CAAGAGACTCAGATA 2778  
 RESULT 4  
 AK034276 3097 bp mRNA linear HTC 05-DEC-2002  
 LOCUS AK034276  
 DEFINITION Mus musculus adult male diencephalon cDNA, RIKEN full-length  
 TUMOR ASSOCIATED PROTEIN NAG14 [Homo sapiens], full insert  
 sequence.  
 ACCESSION AK034276  
 VERSION AK034276.1 GI:26329834  
 KEYWORDS HTC; CAP trapper.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 REFERENCE  
 AUTHORS Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636  
 REFERENCE  
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20493374  
 PUBMED 11042159  
 REFERENCE  
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
 Kono, H., Akiyama, J., Nishi, K., Kutsuna, T., Tashiro, H., Itoh, M.,  
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,  
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 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system-384-format



Db 1555 TTGAAAGGCTTTCATACATCTCAGAAAGGTCCTTGAAGGTCCTGTCATCTGAGAT 1614  
 Qy 201 LeuAsnLeuGlyMetCysAsnIleLeuAspMetProAsnLeuThrProLeuValGlyLeu 220  
 Db 1615 TTGAACCTTGGCCATGGCAACCTTGGGAATCCCTTAACCTTCACACACCTCATCAACT 1674  
 Qy 221 GUGUGLeuGluMetSerGlyAsnHisPheProGluIleArgProGlySerPheHisGly 240  
 Db 1675 GACGACCTAGATCTTCTGGGAACATTTGTGTGCATACAGGCTGCTTTTCAGGGG 1734  
 Qy 241 LeuSerSerLeuValSerLeuThrValMetAsnSerGlnValSerLeuIleGluAsn 260  
 Db 1735 TTGATCACCCTTCAAAACCTGTGATGATACAGTCTCAGATTCAGTCTTGAACCGAAT 1794  
 Qy 261 AlaPheAspGlyLeuValSerLeuValGluLeuAsnLeuAlaHisAsnMetLeuSerSer 280  
 Db 1795 GCTTGTGATACCTTCAGTCTAGTGGAGATTAACCTGGCACACACAACTTAACATTA 1854  
 Qy 281 LeuProHisAspLeuPheThrProLeuArgTyrrLeuValGluLeuHisHisAsn 300  
 Db 1855 TTGCTCATGACCTCTTCACACACCTTGCATCATCTGAGAGATACACCTCCATCAAC 1914  
 Qy 301 ProTyrrAsnCysAspCysAspIleLeuThrProLeuAlaTrpTyrrLeuArgGluTyrr 320  
 Db 1915 CCGTGAACCTGTAACCTGTATATCTGTGGCTCAGCTGTGATGAAGACATGGCCCC 1974  
 Qy 321 ThrAsnSerThrCysCysGlyArgCysHisAlaProMetHisMetArgGlyArgTyrrLeu 340  
 Db 1975 TCCACACACAGCTTGTGTGCCAGGTGTAAACCTCCCACTGAAAGGAGGTATCATC 2034  
 Qy 341 ValGluValAspGlnAlaSerPheGlnCysSerAlaProPheIleMetAspAlaProArg 360  
 Db 2035 GGAAGACTGACCAAGATTAATCTTACATGCTATGCTCCCTAATTGGAGCCCCCTGCA 2094  
 Qy 361 AspLeuAsnIleSerGluGlyArgMetAlaGluLeuLeuCysArg--ThrProMet 379  
 Db 2095 GACCTCATATCTCATGTAAGGCATAGCGAGCTGACCTGAAAGTGGCGCTTCTACGCTCC 2154  
 Qy 380 SerSerValTyrrProLeuLeuProAsnGlyThrValLeuSerHisAlaSerArgHisPro 399  
 Db 2155 ACTTCGATCTTGGATTAATCTCAAAATGAAGACGTGACCCACGGGAGATCAAAAGT 2214  
 Qy 400 ArgIleSerValLeuAsnAspGlyThrLeuAsnPheSerHisValLeuLeuSerAspThr 419  
 Db 2215 CGGATAGCTGTGCTGACCGACCGATCTTAATTTCAATGAATGATGTGCAAGCAC 2274  
 Qy 420 GlyValTyrrCysMetGlyThrAsnValAlaGlyAsnSerAsnAlaSerAlaTyrrLeu 439  
 Db 2275 GGCATGTACACATGATGATGTGATGATTTCTGTGGCAACACCACTGCTTGCACCTTG 2334  
 Qy 440 AsnGlySerThrIleGluLeuAsnThrSerAsnTyrrSerPhePheThrArgTyrrGly 459  
 Db 2335 AATGTTACTCGGCA-----ACCACATCTCCGCTTCTGATCTTTCACCTGTAACGTGA 2388  
 Qy 460 GluThrThrGluIleSerProGluAsp-----ThrIleArgTyrrGlySerProVal 476  
 Db 2389 GAAACTGTGAACCTTCTCAGATGAGACGACGACCAACATGAATGATGGGCCACT 2448  
 Qy 477 Pro-----ThrIleSerThrGlyTyrrGlnProAlaTyrrThrSerThr 491  
 Db 2449 CCAAGTATCATGATGGAGACCAACCAATGA-----ACCACATCTCTT 2490  
 Qy 492 ThrValLeuIleGlnThrThrArg--ValProIleGlnValAlaValProAlaThrAsp 510  
 Db 2491 ACCGCA-----CAGACACAAAGGTGCACAGAAAAAACATTCACCACTCCAGTAACGAC 2544  
 Qy 511 ThrThrAspLeuMetGlnThrSerLeuAspGluValMetIleThrThrIleIleIle 530  
 Db 2545 ATCAACAGCGGAATC-----CAGAAATTTGATGAGTCTGAAAAACATTAATCATTAAT 2601  
 Qy 531 GlyCysPheValAlaValThrLeuLeuAlaAlaMetLeuIleValPheTyrrLeu 550  
 Db 2602 GGGGTTTGTGGCATCACATCATGCTGCGTGTGATGCTGCTCATTTCTCAAGATG 2661

Qy 551 ArgIleArgHisGlnGlnArgSerThrValThrAlaAlaArgThrValGluIleGln 570  
 Db 2662 AGGAACAGCAGCCATCGGCAAAACACATGCTCCACAGAGACTGTGAATCATTAAC 2721  
 Qy 571 ValAspGluAspIleProAlaAlaThrSerAlaAlaAlaThrAlaAlaProSerGlyVal 590  
 Db 2722 GTGATGATGATGATCATCGGGGACAGCCCATG----- 2754  
 Qy 591 SerGlyGluGlyAlaValValLeuProThrIle---HisAspHisIleAsn---TyrAsn 608  
 Db 2755 -----GAAAGCCACTGCGCATGCTGTGATGATGAGCATGAGCACCCTAAACCTATAC 2808  
 Qy 609 ThrTyrrProAlaHisGlyAlaHisTrpThrGluAsnSerLeuGlyAsnSerLeuHis 628  
 Db 2809 TCTTCAAAATCTCCCTTCAACACACACAAACAGTAACACATTA---ATTCAATATAC 2865  
 Qy 629 ProThrValThrThrIleSerGluProTyrrIleIleGlnThrHisThrLeuAspTyrrVal 648  
 Db 2866 -----AGTTCAGTGCATGAACCGTTATGATCGAATGAATGAATGAACATGTA 2916  
 Qy 649 GlnGluThrGlnIle 653  
 Db 2917 CAAGAGACTCAGATA 2931  
 RESULT 5  
 AK048322  
 LOCUS  
 DEFINITION  
 AK048322 3133 bp mRNA linear HTC 05-DEC-2002  
 Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched  
 library, clone: C130049F17 product: weakly similar to BRAIN Tumor  
 ASSOCIATED PROTEIN NAG14 [Homo sapiens], full insert sequence.  
 ACCESSION  
 VERSION  
 AK048322.1 GI:26339261  
 KEYWORDS  
 HTC; CAP trapper.  
 SOURCE  
 Mus musculus (house mouse)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 REFERENCE  
 AUTHORS  
 1 Carninci, P. and Hayashizaki, Y.  
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 JOURNAL  
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 REFERENCE  
 AUTHORS  
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 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
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 Kono, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,  
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,  
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 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer  
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 JOURNAL  
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 20530913  
 PUBMED  
 11076861  
 REFERENCE  
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 4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,  
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 Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Cabavani, T.,  
 Fleischmann, W., Gasteirland, T., Gissi, C., King, B., Kocchiwa, H.,  
 Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G.,





QY	281	LeuProHisAspLeuPheThrProLeuArgTyrLeuValGluLeuHisLeuHisAspN	300
DB	2024	TTGCTTCAATGACCTTCTTCAACACCTTGATATATCTAGAGAGATATACCTTCATCACAC	2083
QY	301	ProTyrAsnGlyAspGlyAspIleLeuTyrLeuValATyrTyrLeuArgGluTyrIlePro	320
DB	2084	CCGGTGAACCTGTAATCTGTGATATCTGTGGCTCAGCTGTGGATGAAGAATGAGACATGGCCCC	2143
QY	321	ThrAsnSerThrGlyGlyGlyValArgGlyHisIleAspMetHisMetArgGluArgTyrLeu	340
DB	2144	TTCAACACAGACTGTGCTGTGCCAGGTTGATACACTCCGCCCAACTGAAAGGAGGATACATC	2203
QY	341	ValGluValAspGlnAlaSerPheGlnGlySerAlaProPheIleMetAspAlaProArg	360
DB	2204	GGAAGAGCTGACCAAGAAATTACTTTATCATGCTATGCTCCGTAATGTGTGAGACCCCTGCA	2263
QY	361	AspLeuAsnIleSerGlnGluValArgMetAlaGluLeuGlyGlyAspGlyValGlyProMet	379
DB	2264	GACCTCAATGTCATCGAAGGACATGGCACCTGAGCTGAATATCGGGCTTCACTGCTCCTG	2323
QY	380	SerSerValIleTyrPheLeuProAsnGlyThrValLeuSerHisIleSerArgHisPro	399
DB	2324	ACTTCGCGATCTGTGATTACTCCAAATGGAACAGTCAAGACCCACGGGGCATCAAACTG	2383
QY	400	ArgIleSerValLeuAsnAspGlyThrLeuAsnPheSerHisValLeuLeuSerAspThr	419
DB	2384	CGGATAGCTGTGCTCAGCGACGGGTCTTTAAATTCACAAATGTATCATGTCTCAAGACACA	2443
QY	420	GlyValIleTyrThrCysMetGlyThrAsnAlaAlaGluAsnSerAsnAlaSerAlaTyrLeu	439
DB	2444	GGCATGTACACATGTATGATGTGGTAATCTGTGGCAACACCATGCTTCTGCACTTG	2503
QY	440	AsnGlySerThrAlaGluLeuAsnThrSerAsnTyrSerPhePheThrThrGlyThrGly	459
DB	2504	AATGTACTCGGGCA-----ACCATCTACCTCGTTCTGTATCTTTCAACTGTAACTGAT	2557
QY	460	GluThrThrGluIleSerProGluAsp-----ThrThrArgGlyTyrGlyProVal	476
DB	2558	GAGACTATGAGAACTTCTTCAGATATAGGACCGGACACACAGATTAACATGTGGGCCCACT	2617
QY	477	Pro-----ThrThrSerThrGlyTyrGlnProAlaTyrThrThrSerThr	491
DB	2618	CCAAGTATGCATGGGAGACACCACTGTA-----ACCACATCTCTT	2658
QY	492	ThrValIleuIleGlnThrThrArg--ValProGlyGlnValAlaValProAlaThrAsp	510
DB	2660	ACGCCA-----CAAGACACAAGGTGCGACAGAAAAAATTCCACCATCCCATGTAATCAGC	2713
QY	511	ThrThrAspIleMetGlnThrSerLeuAspGluValMetGlyThrThrGlyIleIleIle	530
DB	2714	ATCAACACGGCGAATC---CCAGGAATTGATGGGTCATGAAACATCACTTAATCATTTT	2770
QY	531	GlyCysPheValAlaValThrLeuLeuAlaAlaMetLeuIleValPheTyrIleLeu	550
DB	2771	GGGTGTTTGTGGCATACACTGATGCTGCGGATGCTGATGCTGATTTTCTACAAGATG	2830
QY	551	ArgGlyValArgHisGlnGlnArgSerThrValThrAlaAlaArgHisValGluIleIleGln	570
DB	2831	AGGAACAACGACCATCGGCAAAACACCATGCTCCAAACAGGACGTGTGAATCATTTAAC	2890
QY	571	ValAspGluAspIleProAlaIleThrSerAlaAlaIleThrAlaAlaProSerGlyVal	590
DB	2891	GTGGATGATGAGATCACTGGGACACGCCCATG-----	2923
QY	591	SerGlyGlnGluAlaValValLeuProThrIle--HisAspHisIleAsn--TyrAsn	608
DB	2924	-----GAAAGCCACCTGCCCATCGCTGCGATTTGAGCATGAGCACTTAACACCATATTAAC	2977
QY	609	ThrTyrLeuValProAlaHisGlyAlaHisIleTyrThrGluAsnSerLeuGlyAsnSerLeuHis	626
DB	2978	TCTTACAAATCTCCCTTCAACACACAAACAAAGTAAACAAATC---AATTCATATAC	3034

Db	Accession	Definition	LOCUS	Result
Oy	629	Prothoracic gland protein, full-length cDNA, RIKEN full-length enriched library, clone:630579019 product:weakly similar to BRAIN TUMOR ASSOCIATED PROTEIN NAG14 (Homo sapiens), full insert sequence.	AKO32088	2873 bp mRNA linear HTC 05-DEC-2002
Db	3035	-----AGTTACGTCATGAACCTTATGTATCCGATGACCTTAAGCAATGTA	AKO32088	3085
Oy	649	Glial fibrin acidic protein, full-length cDNA, RIKEN full-length enriched library, clone:630579019 product:weakly similar to BRAIN TUMOR ASSOCIATED PROTEIN NAG14 (Homo sapiens), full insert sequence.	AKO32088	2873 bp mRNA linear HTC 05-DEC-2002
Db	3086	CAAGAGACTCAGATA	AKO32088	3100
REFERENCE	AKO32088	AKO32088.1 GI:26082676		
VERSION	AKO32088	AKO32088.1 GI:26082676		
KEYWORDS	HTC; CAP trapper.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	Carninci, P. and Hayashizaki, Y.			
AUTHORS	1	High-efficiency full-length cDNA cloning		
TITLE	Carninci, P. and Hayashizaki, Y.			
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)			
MEDLINE	99279253			
PUBMED	10349636			
REFERENCE	2			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)			
MEDLINE	20499374			
PUBMED	11042159			
REFERENCE	3			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitamura, T., Tashiro, H., Itoh, M., Suni, N., Ishi, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kaishiwagi, K., Fujikawa, Y., Inoue, K., Togawa, Y., Iwawa, M., Ohara, E., Matsuura, S., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.			
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer			
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)			
MEDLINE	20530913			
PUBMED	11076861			
REFERENCE	4			
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishi, Y., Aizawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, S., Yamada, S., Aikawa, K., Iwawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L.M., Stambli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Baren, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bulc, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hochmann, M., Hume, D.A., Kamlay, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, C., Seta, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyokawa, K., Wang, K.H., Weitz, C., Wittaker, C., Wilmink, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, J., Kohzuki, S. and Hayashizaki, Y.			
TITLE	Functional annotation of a full-length mouse cDNA collection			
JOURNAL	Nature 409 (6821), 685-690 (2001)			
MEDLINE	21083660			
PUBMED	11217851			



REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
SOURCE  
misc\_feature  
BASE COUNT  
ORIGIN  
Alignment Scores:  
Pred. No.:  
Score:  
Percent Similarity:  
Best Local Similarity:  
Query Match:  
DB:  
US-09-991-053-10 (1-653) x AK032088 (1-2873)

5  
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
(bases 1 to 2873)  
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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirao, T., Hirozane, T., Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, Y., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurahara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku, Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
Direct Submission  
Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.go.jp/  
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REFERENCE
AUTHORS
Molecular, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognath; Muridae; Murinae; Mus.
1 (bases 1 to 1845)
Strasbourg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Sherman, C.M., Schuler, G.D.,
Altschul, S.F., Zieberg, B., Buetow, K.H., Schaefer, C.F., Hsieh, F.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Donald, M.F., Cavallari, T.L.,
Schneitz, T.E., Brownstein, W.J., Uedlin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Mortley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Boutland, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Gilmwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalins, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE
PUBMED
12477932
2 (bases 1 to 1845)
Strasbourg, R.
Direct Submission
Submitted (04-JUN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA.
NIH-MGC Project URL: http://mgc.ncl.nih.gov
Contact: MGC help desk
Email: gcgdb@mail.nih.gov
Tissue Procurement: Gerard Gradwohl (PNAS 97 P1607-1611, 2000)
CDNA Library Preparation: Catherine Lee, Endocrine Pancreas
Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLI)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center.
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louleed, H.,
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Clone distribution: MGC clone distribution information can be found
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 REFERENCE 1 (bases 1 to 1914)  
 AUTHORS Strauberg, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 CONTACT: MGC help desk  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: Life Technologies, Inc.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI)  
 DNA Sequencing by: National Institutes of Health Intramural  
 Sequencing Center (NISC),  
 Gaithersburg, Maryland;  
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 Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,  
 Hansen, N., Ho, S.-L., Karlins, B., Kwong, P., Latic, P., Legaspi, R.,  
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AUTHORS	Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Chen, J., Chen, Z. and Han, Z.		
TITLE	Homo sapiens cDNA ADC clones		
JOURNAL	Unpublished		
COMMENT	Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919 (ex. 45) Fax: 86-21-50801922 Email: hanzg@chgc.sh.cn This clone is available at CHGC in Shanghai.		
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Qy	189	GluGlyAlaPheGluGlyLeuPheAsnLeuArgTyrLeuAsnLeuGlyMetCysAsnIle	208
Db	122	GAGGAGAGCTTTGAGGGGCTGTTCACCTCAAGTATCTGAATCTGGGCATGTGCACACTT	181
Qy	209	LysAspMetProAsnLeuThrProLeuValGlyLeuGluGluLeuGluMetSerGlyAsn	228

Db	182	AAAGACATGCCAATCTCACCCCCCTGTGGGCGTGAAGAGCTGGAGANTGCAGGGAAC	241
Oy	229	HispheProGUluleahgProgiYserPheniGLyleuSerleUlyslvleUtp	248
Db	242	CAC TTCCTCCTAGATCAAGACAGCCCTGGCTCTTCCTCATGGCTTGAGCTCCCTCAAGAAGCTCTGG	301
Oy	249	VAlMeIarSenSergInVAsISerLeuIlleGlUnArASnAlaphEapSpGIyleUlAIsErLeu	268
Db	302	GTCATGAACCTCACAGGCTCAGCTGATTGAGCGGATCTTTTGACGGGACTGGCTTCACTT	361
Oy	269	VAlGluleuAnSleuAlaNIasnasnleuSerSeurHeuProHisApLeuPethrPro	288
Db	362	GTGGAAC TCAACTGGGCCACAATAAACCTCTCTTTGGCCCCATGACCTTTTAACCCCG	421
Oy	289	LeuArGYrleuValGluleuHIsleUHIsIHIsanPProTrphancYsaAPCySaPIle	308
Db	422	CTGAGGTAACCTGGTGGAGTTGACATCTACACCACACACCTTGAACTGTGATTGACATT	481
Oy	309	LeuTrpleuAlatPrTpLpleuArGluTyrlleProthrAnseerThrcysGlgIYArg	328
Db	482	CTGGGCTCAGCTGGTGGCTTCGAGAGTATATCCCAACCAATTCACCTCTGTGGCGCG	541
Oy	329	CysHisAlaPromethismetArGGLYArgTYrleuValGluleuAspGINalaserPhe	348
Db	542	TGTATGCTCCCATGACATGACGAGCGCGGTACTCTGT - GAGGTGAGCACAGCCTTTT	600
Oy	349	GLncYSserAlaPropheIIemelaspAlaProArGspLeuanIllesergJugIYArg	368
Db	601	CAGGCTCTTGCCCTTCATCATGAGCAGCACTTGAGACCTCAACATTTCTGAGGGGCGG	660
Oy	369	MelAlagIleuUlysCYsArg-ThrProPrometSerSevallystrpleuUen-ProA	388
Db	661	ATGGCACAACCTTAGTGCGGGAATCTCCCTTAAGCCTCCGCGAAGGTGTCGGCCA	720
Oy	388	sngIYThrValleuSenHIsAlaserRghIsPProArGIlleSeValleuAnsnApGIYT	408
Db	721	TTGGGACCCGtggTAAcAcAGcCTTCCGcAcCCAcAGAtCTTCTGcCTAAAcAGGgGA	780
Oy	408	hrleuAnsnphe 411	
Db	781	CTTTGACCTT 791	
RESULT 10			
LOCUS	BC019687	1303 bp	mRNA linear HTC 01-MAY-2002
DEFINITION	Homo sapiens, clone IMAGE:4941836,		mRNA.
ACCESSION	BC019687		
VERSION	BC019687.2	GI:20380048	
KEYWORDS	HTC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 1303)		
JOURNAL	Strausberg,R. Direct Submission Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	On May 1, 2002 this sequence version replaced gi:18044633. Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: David N. Louis, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.W.A.G.E. Consortium (ULNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amg@bcm.tmc.edu Guarnatne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,		

Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,  
Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/ILM, at: <http://image.llnl.gov>  
Series: IRK Plate: 29 Row: P Column: 15  
This clone was selected for full length sequencing because it  
passed the following selection criteria: Similarity but not  
identity to protein  
This clone has the following problem: no polyA-tail.

## FEATURES

## source

Location/Qualifiers  
1..1303  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4941836"  
/issue\_type="Brain, anaplastic oligodendroglioma with  
1p/19q loss"  
/clone\_id="NCI CGAP\_Brn67"  
/lab\_host="DH10B"  
/note="Vector: pCMV-SPORT6"  
BASE COUNT 233 a 476 c 405 g 189 t  
ORIGIN

## Alignment Scores:

Pred. No.: 1,11e-109 Length: 1303  
Score: 1169.00 Matches: 228  
Percent Similarity: 67.99% Conservative: 63  
Best Local Similarity: 53.27% Mismatches: 99  
Query Match: 33.92% Indels: 38  
DB: 11 Gaps: 5

US-09-991-053-10 (1-653) x BC019687 (1-1303)

QY 197 Aenleuetyrteuennleuglymetcyaaenlleayaspmetproanleuthrpro 216  
DB 15 AACCTCGGCTCACTCACTGGGATGTGCACCTCAAGACATCCCACTGACGGCC 74  
QY 217 LeuValGlyLeuGluGluLeuGluMetSerGlyAenHiePheProGluLeuArgProGly 236  
DB 75 CTGGTCGGCTGGAGAGAGCTGTGTGGGCGAACCGGCTGACCTGATCCCGCGGCG 134  
QY 237 SerPheHieGlyLeuSerSerLeuGlyLeuTyrValMetAenSerGlnValSerLeu 256  
DB 135 TCCCTTCAGAGGTCTCAACGAGCTGCGCAAGCTGTGCTATGACGCCAGGAGCCACC 194  
QY 257 TleGluArgAenAlaPheArgGlyLeuAlaSerLeuValGluLeuAenAlaHieAen 276  
DB 195 ATCGAGCGCAACCGCTTGCAGACGCTCAAGTGGCTGAGAGAGCTCAACCTGTCCACAC 254  
QY 277 AenLeuSerSerLeuProHieAenPheThrProLeuArgTyrLeuValGluLeuHie 296  
DB 255 AACCTATGTGCTGCTCCCAACGACCTTTCACGCGCTGACCGGCTCGAGCGCGGCAC 314  
QY 297 LeuHieAenProTyrPheAnCyaaPcyaaPheLeuTyrPheAlaTyrPheLeuArg 316  
DB 315 CTCAACCAACAACCGCTGCACTTGCAGAGTGTGCTGCTGAGTGTGCTGCTCAAG 374  
QY 317 GluTyrIleProThrAenSerThrCyaaGlyArgCyaaHieAlaProMetHieMetArg 336  
DB 375 GAGAGCGTCCCGCAACGACGAGTGTGCGCGGTGTCAATGCGCGCGCGCGCAAG 434  
QY 337 GlyArgTyrLeuValGluValAenGlnAlaSerPheGlnCyaaSerAlaProPheIleMet 356  
DB 435 GGGCGCTAATTTGGAGAGCTGAGCCAGTGTGCTTCACTGCTATGCGCGCTCATGCG 494  
QY 357 AenAlaProArgAenPheAenHieSerGlnArgMetAlaGluLeuArgCyaaArgThr 376  
DB 495 GAGCGCGCCAGCGGACCTCAACGACGAGGAGTGTGCGAGTCAAAATGCGCGCAG 554  
QY 377 ---ProPheMetSerSerValTyrPheLeuProArgGlyThrValLeuSerHieAla 395  
DB 555 GGCACCTCATGACCTTCGTCACCTGTGACCGCCCAAGGAGCACTCATGACCGCAGCG 614

QY 396 SerArgHieProArgIleSerValLeuAenArgGlyThrLeuAenPheSerHieValLeu 415  
DB 615 TCTTACCGCGGCGGATCTCCGCTCTGATGACGCGCACGCTTAATTCACCAAGCTCAC 674  
QY 416 LeuSerAenPheArgValTyrThrCyaaMetGlyThrAenValAlaGlyAenSerAenAla 435  
DB 675 GTCGAGGACAGCGGCGCAATCAACGTCATGTGTGACGAACTGACCGCGCACACCGCC 734  
QY 436 SerAlaTyrLeuAenGlySerThrAlaGluLeu 446  
DB 735 TCGGACGCTTCAACGCTTCCGCGCTGACCCCGTGGCGCGCGGCGCACCGGACCGCC 794  
QY 447 -----AenThrSerAenTyrSerPhe 454  
DB 795 GGGGCGCGGCGCTGGGCGAGTGTGTGTGTGAGGCGGCGAGTGGCGGCTACACCTACTTC 854  
QY 455 ThrThrGlyThrGlyGluThrThrGluLeuSerProGluAenPhe 469  
DB 855 ACCAGCGTGTGAGAGACCTGAGACGCGAGCGCGAGAGAGAGCGCCCTGACGCGCGG 914  
QY 470 ---ThrArgTyrTyrLeuProValProThr 479  
DB 915 GGGAGCGAGAGAGAACCGCGAGGCTCCAGACAGGTGTCTGGGCTGGGCGCGGCT 974  
QY 480 SerThrGlyTyrGlnProAlaTyrThrSerThrThrValLeuIleGlnThrArg 499  
DB 975 GGGGAGCGGCGCGCGCGCTCGCTCGCTTCAACAGCGACCGCGCGCGCTCGCGCGG 1034  
QY 500 ---ValProGlyGlnValAlaValProAlaThrAenPheThrAenPheMetGlnThrSer 518  
DB 1035 CCCAGGAGAGAGCGCTTCAACGCTGCGCATCAAGATGTGACGAGCGACCGCTCAAGAC 1094  
QY 519 LeuAenGluValMetLeuThrThrTyrIleIleGlyCyaaPheValAlaValThrLeu 538  
DB 1095 CTGAGAGAGTATGAAACCAACCAAAATCAATCGGCTCTTGTGCGCATCACTTC 1154  
QY 539 LeuAlaAlaAlaMetLeuIleValPheTyrLeuAenTyrLeuArgHieGlnArgSer 558  
DB 1155 ATGGCGCGGAGTGTGTGTGTGCTTCAACAGCTGCGCAAGCACAGCTCCACAG 1214  
QY 559 ThrValThrAlaAlaArgThrValGluIleIleGlnValAenGluAenPheProAlaAla 578  
DB 1215 CACCAAGCGCGCGCGCGCGAGCTGAGATCATCAACGAGAGAGAGAGCTCCGCGCGC 1274  
QY 579 ThrSerAlaAlaAlaThrAlaAla 586  
DB 1275 TCGGCGGTGTGCGTGGCGCGCG 1298

RESULT 11  
BX460831 913 bp mRNA linear EST 22-MAY-2003  
LOCUS BX460831 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone  
DEFINITION CS0DF019Y003 5-PRIME, mRNA sequence.  
ACCESSION BX460831  
VERSION BX460831.1 GI:31023277  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 913)  
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: [segreg@genoscope.cns.fr](mailto:segreg@genoscope.cns.fr), Web: [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 9423.r  
more information about this cluster, see  
<http://www.genoscope.cns.fr/>





## ORIGIN

## Alignment Scores:

Pred. No.: 1, 71e-99 Length: 845  
 Score: 1067.50 Matches: 197  
 Percent Similarity: 84.59% Conservative: 39  
 Best Local Similarity: 70.61% Mismatches: 42  
 Query Match: 30.98% Indels: 2  
 DB: 13 Gaps: 1

US-09-991-053-10 (1-653) x BU706148 (1-845)

QY 135 LeuThrValIleProSerGlyAlaPheGluTyrLeuSerIleuArgGluLeuTyrLeu 154  
 10 CTGACACCGGTGCCCGCAGCGCTTGTAGTACCTGTCCAGCTCCGAGAGCTGTGGCTG 69  
 QY 155 ArgAsnAspProIleGluSerIleProSerTyrAlaPheAsnArgValProSerLeuMet 174  
 70 CGCAACACCCCGATCCAAAGCATCCATGCTTCAACCGTGTGCCCTCAGCTGGCG 129  
 QY 175 ArgLeuAspLeuGlyGluLeuGlyLeuGluTyrIleSerGluGlyAlaPheGluGly 194  
 130 CGCTTACAGCTGGGCGACGCTGAAAGAGCTGAGTACATATCTGAGGCGGCTTCGAGGG 189  
 QY 195 LeuPheAsnLeuGlyTyrLeuAsnLeuGlyMetCysAsnIleLysAspMetProAsnLeu 214  
 190 CTGGTGAACCTGGCTACCTCAACCTGGGCACTGTGCACTTAAGACATCCCAACCTTC 249  
 QY 215 ThrProLeuValGlyLeuGluGluLeuGluMetSerGlyAsnHisPheProGluIleArg 234  
 250 ACAGCACTGTGTGGCTGTGAGAGCTGAGACTCTCCGGGAAACCGGCTGACCTTAATTCG 309  
 QY 235 ProGlySerPheHisGlyLeuSerSerLeuLeuGlyLeuTyrValMetAsnSerGluVal 254  
 310 CTGGCTCTCTTCCAGGGCTCACACGCTTCGCAAGCTGTGGCTGATGCCCAAGT 369  
 QY 255 SerLeuIleGluArgAsnAlaPheAspGlyLeuAlaSerLeuValGluLeuAsnLeuAla 274  
 370 GCCACCATCGAGGAAACGCTTCGAGACCTCAAGTGGCTGAGAGAGCTGAACCTGTGCC 429  
 QY 275 HisAsnAsnLeuSerSerLeuProHisAspLeuPheThrProLeuArgTyrLeuValGlu 294  
 430 CACAAACACCTGATGTGCTGCGCGACGACCTTTTACCGCCCTTCACCGCTGAGCGT 489  
 QY 295 LeuHisLeuHisHisAsnProTyrAsnAspCysAspIleLeuTyrLeuAlaTyrTyr 314  
 490 GTCCACTGAAACCAACACCCCTGACATGTGATGTGCTGTGGCTGACCTGATG 549  
 QY 315 LeuArgGluTyrIleProThrAsnSerThrCysCysGlyArgCysHisAlaProMetHis 334  
 550 CTGAAGAGACAGTGGCCGACCAATCAACATGTGGCGACGCTGCCACCGCGCGCGCG 609  
 QY 335 MetArgGlyArgTyrLeuValGluValAspGluAlaSerPheGlnCysSerAlaProPhe 354  
 610 CTCAAGGCGCGTACATTTGGCGAGCTAGACAGTGCACCTTCATGTGCCCCGATC 669  
 QY 355 IleMetAspAlaProArgAspLeuAsnIleSerGluGlyArgMetAlaGluLeuLysCys 374  
 670 ATGTGAGGCCACACAC-GACCTCAATGTACCGAGGCGATGGCGGTGAGCTCAAGTGT 728  
 QY 375 ArgThr--ProPheMetSerSerValIleTyrLeuLeuProAsnGlyThrValLeuSer 393  
 729 CGCACAGGACATCCATCGATGAGTGGTCAACTGGCTGACACTTAACGCGACGCTCATGAG 788  
 QY 394 HisAlaSerArgHisProArgIleSerValLeuAsnAspGlyThrLeuAsnPheSer 412  
 789 CACGGTTCCTATGTGTGTGCGCATTTCTGCTGCACAGATGGACACTCAACTTCACCC 845

## RESULT 13

BI916800 803 bp mRNA linear EST 16-OCT-2001  
 LOCUS 60317924F1 NIH\_MGC\_121 Homo sapiens cDNA clone IMAGE:524228 5',  
 DEFINITION mRNA sequence.

ACCESSION BI916800  
 VERSION BI916800.1 GI:16180754  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 803)  
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Stransberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: Life Technologies, Inc.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLN at:  
<http://image.llnl.gov>  
 Plate: L16M1610 row: P column: 05  
 High quality sequence stop: 795.  
 Location/Qualifiers

## FEATURES

## source

1..803  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:524228"  
 /lab\_host="DH10B"  
 /clone\_11b="NIH\_MGC\_121"  
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: EcoRV (destroyed); RNA source anonymous pool of 3  
 fetal brains, female age 20 weeks, female age 24 weeks,  
 and male age 26 weeks. Library is oligo-dT primed and  
 directionally cloned (EcoRV site is destroyed upon  
 cloning). Average insert size 1.7 kb, insert size range  
 0.7-3.5 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genes tracking code 017. Note:  
 this is a NIH MGC Library."

BASE COUNT 146 a 290 c 233 g 134 t  
 ORIGIN

## Alignment Scores:

Pred. No.: 5.35e-97 Length: 803  
 Score: 1043.00 Matches: 193  
 Percent Similarity: 86.03% Conservative: 36  
 Best Local Similarity: 72.56% Mismatches: 36  
 Query Match: 30.27% Indels: 2  
 DB: 12 Gaps: 0

US-09-991-053-10 (1-653) x BI916800 (1-803)

QY 93 AspThrPheArgHisLeuHisIleLeuGluValLeuGluIleGlyArgAsnSerIleArg 112  
 1 GACAGCTTCAACACCTGGGCACTGGAGATTGACAGCTGAGCAAGACCTGTGGCG 60  
 QY 113 GlnIleGluValGlyAlaPheAsnGlyLeuAlaSerLeuSerThrLeuGluLeuPheArg 132  
 61 AAGATCGAGGTGGGCGCTTCAACGGGCTGCCACACCTCAACACCTGAGCTTTTATAC 120  
 QY 133 AsnTyrLeuThrValIleProSerGlyAlaPheGluTyrLeuSerIleuArgGluLeu 152  
 121 AACCGGCTACACGAGTCCACGAGGCTTCGAGTACCTGTCCAAAGCTGGGAGACTC 180  
 QY 153 TrpLeuArgAsnAspProIleGluSerIleProSerTyrAlaPheAsnArgValProSer 172  
 181 TGGCTGGGAAACACCCATCGAGAGCATCCCTCTACGCTTCAACCGGCTGCCCTCG 240  
 QY 173 LeuMetArgLeuAspLeuGlyGluLeuGlyLeuGluTyrIleSerGluGlyAlaPhe 192  
 241 CTGGCGCGCTGGACCTGGGCGAGCTCAAGCGGCTGGAATACATCTCGAGGCGGCTTC 300



QY 193 GUGUgLeuPheAsnLeuLysTyrLeuAsnLeuGlyMetCysAsnIleLysAspMetPro 212  
 Db 301 GAGGGGCTGGTCAACCTGCTACCTCAACCTGGGCGATGTGCACTCAAGACATCCCC 360  
 QY 213 AsnLeuThrProLeuValGlyLeuGluLeuGluMetSerGlyAsnHisPheProGlu 232  
 Db 361 AACCTGAGCGGCTGGTGGCTGGAGGCTGGAGCTGTCCGGCAACCGGCTGGACCTG 420  
 QY 233 IleATGProGlySerPheHisGlyLeuSerSerLeuLysLysLeuThrValMetAsnSer 252  
 Db 421 ATCCGCGGCGGCTCTTCCAGGAGTCTCACACAGCTGCGGACCTGTGGCTCATGCAAGCC 480  
 QY 253 GlnValSerLeuIleGlnLysAsnAlaPheAspGlyLeuAlaSerLeuValGluLeuAsn 272  
 Db 481 CAGGTAGCCACCATGAGCGCAACCGCTTCCAGCACTCAAGTCCCTGGAGAGAGCTCAAC 540  
 QY 273 LeuAlaHisAsnAsnLeuSerSerLeuProHisAspLeuPheThrProLeuArgTyrLeu 292  
 Db 541 CTGTCCCAACMAACCTGATGTGTGCTGCCCAAGACCTCTTCAAGCCCTGCAAGCCGCTC 600  
 QY 293 ValGluLeuHisLeuHisAsnProThrAsnCysAspCysAspIleLeuThrLeuAla 312  
 Db 601 GAGCGGCTGACCTTCAACCAACACCTGCGCATGTGCATGCAAGCTGTGGCTGAGAGC 660  
 QY 313 TrpTrpLeuArgGluTyrIleProThrAsnSerThrCysCysGlyArgCysHisAlaPro 332  
 Db 661 TGGTGGCTCAAGAGAGCGGTGCCCAAGCAACGACGTGTGCGCCGCTGTATGAGGCC 720  
 QY 333 MetHisMetArgGlyArgTyrLeuValGluValAlaAspGlnAlaSerPheGln-CysSerAl 352  
 Db 721 GC-CGCGCTCAAGGGGGCTACATGTGGGAGCTGACACAGTCCCAATTCACCTGATATGC 779  
 QY 352 AProPheIleMetAsp 357  
 Db 780 GCCCGTCATGTGAG 795  
 RESULT 14 870 bp mRNA linear EST 06-JAN-2003  
 LOCUS CA978880  
 DEFINITION AGENCOURT\_11277140 NIH\_MGC\_164 Mus musculus cDNA clone  
 IMAGE:30143630 5', mRNA sequence.  
 CA978880  
 ACCESSION CA978880.1 GI:27511534  
 VERSION EST.  
 KEYWORDS  
 SOURCE Mus musculus (house mouse)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 870)  
 AUTHORS NIH-MGC http://img.ncl.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgsabers-rc@mail.nih.gov  
 Tissue Procurement: Dr. David Rowe and Dr. Mina  
 cDNA Library Preparation: Invitrogen Corp  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: NDAM0054 row: m column: 15  
 High quality sequence stop: 610.  
 Location/Qualifiers  
 1..870  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:30143630"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_11b="NIH\_MGC\_164"  
 /note="Vector: PCMV-SPORT6.1.cdb; Site 1: EcoRV; Site 2:  
 NotI; Non-normalized full-length enriched library from

pooled mouse embryonic limb, maxilla and mandible, day  
 10.5 and 11.5 (size selected for the 0.5-1 kb fragments)  
 Cloned directionally, priming method: Oligo-dT. cDNA  
 enrichment: >1k bp, Average insert size 1.8k bp. Priming  
 sequence: 5'-GACTGTTCTTACATGCGGAGCGGCGCTT 3'. Tissue  
 contributed by, David Rowe. Library constructed by Resgen,  
 Invitrogen Corp."

BASE COUNT 174 a 305 c 230 g 161 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 2,54e-96 Length: 870  
 Score: 1037.00 Matches: 192  
 Percent Similarity: 80.62% Conservative: 41  
 Best Local Similarity: 66.44% Mismatches: 50  
 Query Match: 30.09% Indels: 6  
 DB: 14 Gaps: 3

US-09-991-053-10 (1-653) x CA978880 (1-870)

QY 135 LeuThrValIleProSerGlyAlaPheGluTyrLeuSerLysLeuArgGluLeuThrLeu 154  
 Db 6 CTGACACCGGCTCCACGAGGCTTTAGTACCTGTCCAGCTCCGGAGCTGTGGCTG 65  
 QY 155 ArgAsnAsnProIleGluSerIleProSerTyrAlaPheAsnArgValProSerLeuMet 174  
 Db 66 CGCAACACCCCATGAGAGCATCCCATCTTATGCTTCAACCGGTGCTCTCATGCGC 125  
 QY 175 ArgLeuAspLeuGlyGluLeuLysLysLeuGluTyrIleSerGluGlyAlaPheGluGly 194  
 Db 126 CGCCTTAGACCTGGGGGAGACTGAGAGAGCTGAGTACATATCTGAGGCGGCTTGCAGGGG 185  
 QY 195 LeuPheAsnLeuLysTyrLeuAsnLeuGlyMetCysAsnIleLysAspMetProAsnLeu 214  
 Db 186 CTGTGAACTGGCGCTACCTCAACCTGGGCGATGTGCACCTTAAGAGACATCCCAACTC 245  
 QY 215 ThrProLeuValGlyLeuGluGluLeuGluMetSerGlyAsnHisPheProGluIleArg 234  
 Db 246 ACAGCATTTGTGGCTGAGAGAGCTGAGCTGTCCGGAAACCGGCTGAGACTTAATTTGC 305  
 QY 235 ProGlySerPheHisGlyLeuSerSerLeuLysLysLeuThrValMetAsnSerGlnVal 254  
 Db 306 CTGGCTCTCTTCCAGGGGCTCTCACAGCTGGCGAAGCTGTGGCTGATGATGCCCAAGTG 365  
 QY 255 SerLeuIleGluValGlnAsnAlaPheAspGlyLeuAlaSerLeuValGluLeuAsnLeuAla 274  
 Db 366 GCCACCATCGAGCGAAGAGCTTGCAGCACTCAAGTCTGGAGAGACTTAACCTGTGCC 425  
 QY 275 HisAsnAsnLeuSerSerLeuProHisAspLeuPheThrProLeuArgTyrLeuValGlu 294  
 Db 426 CACACACCTGATGTCTGCTGCCGACGACCTTTTCAAGCCCTTCAAGCCCTGAGGCT 485  
 QY 295 LeuHisLeuHisAsnProThrAsnCysAspCysAspIleLeuThrLeuAlaTrpTrp 314  
 Db 486 GTCCACCTGAAACCAACACCTGCGCATGTATGATGTGTGCTGCTGAGCTGAGTGG 545  
 QY 315 LeuArgGluTyrIleProThrAsnSerThrCysCysGlyArgCysHisAlaProMetHis 334  
 Db 546 CTGAAGGAGAGACAGTCCAGCAATACCAATGCTGGCAGCCTGCGACGCGCCCGCGC 605  
 QY 335 MetArgGlyArgTyrLeuValGluValAlaAspGlnAlaSerPheGlnCysSerAlaProPhe 354  
 Db 606 CTCAGAGGCGGCTATTTGGCGAGCTTACAGCTGCACTTCACTGCTATGAGCCGCTC 665  
 QY 355 IleMetAspAlaProArgAspLeuAsnIleSerGluGlyArgMetAlaGluLeuLysCys 374  
 Db 666 ATCTGTGAGGCCCCACAGACTCTCATATGCAACGAGGCGCATAGGCGGTGAGTCAAGTGC 725  
 QY 375 ArgThr---ProProMetSerSerValLysTrpLeuLeuProAsnGlyThrValLeuSer 393  
 Db 726 CGCACAGGACATTCATGATCGGTCAACTGCGTGAACCTTACGAGGACGCTCTGTACC 785  
 QY 394 HisAlaSerArgHisLeuProArgIleSerValLeuAsnAspGlyThrLeu-----Asn 410

Db 786 CACGGTTCTTAT-----CGTGGCGCTTTTCAATGTCACCATTCGCCCACTTACT 839  
 Qy 411 pheSerHisValIleuSerAepThr 419  
 Db 840 TTCACCAATGTCACCGTCCAGGACA 866

## RESULT 15

CA890729

LOCUS CA890729 593 bp mRNA linear EST 20-DEC-2002  
 DEFINITION B0161B05-5N NIA Mouse Neural Stem Cell (Differentiated) cDNA  
 Library (Long) Mus musculus cDNA clone NIA:B0161B05 IMAGE:30099664  
 5', mRNA sequence.

## ACCESSION

CA890729

## VERSION

CA890729.1

## KEYWORDS

EST.

## SOURCE

Mus musculus

## ORGANISM

Mus musculus

## REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 593)

## AUTHORS

Piao, Y., Dudekula, D.B., Qian, Y., Martin, P.R., Alba, K., Vescovi, A.L.  
 and Ko, M.S.H.

## TITLE

Systematic Analyses of NIA Mouse Neural Stem Cell (Differentiated)  
 cDNA Library (Long)

## JOURNAL

Unpublished

## COMMENT

Contact: Dawood B. Dudekula  
 Laboratory of Genetics  
 National Institute on Aging/National Institutes of Health  
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
 Email: cdna@igsun.grc.nia.nih.gov  
 Plate: B0161 row: B column: 05  
 Seq primer: -21M13 Reverse  
 High quality sequence stop: 593  
 POLYA=No.

## FEATURES

Location/Qualifiers

1. 593

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/mol\_type="mRNA"

/strain="CD1"

/db\_xref="taxon:10090"

/clone="NIA:B0161B05 IMAGE:30099664"

/dev\_stage="Adult"

/lab\_host="DH10B"

/clone\_lib="NIA Mouse Neural Stem Cell (Differentiated)  
 cDNA Library (Long)"/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:  
 NotI; Mouse cDNA project by the Laboratory of Genetics,  
 National Institute on Aging (NIA), Intramural Research  
 Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is  
 a long-transcript enriched cDNA library (Ref. Genome Res.  
 11: 1553-1558 (2001). [PMID: 11541991]. Total RNAs were  
 obtained from Dr. Angelo L. Vescovi (Institute for Stem  
 Cell Research, Italy). Double-stranded cDNAs were  
 synthesized with an Oligo(dT) primer [Invitrogen:  
 5'-pGACTAGTCTAGATCGGACGCCGCCCTTTTTTT-3'] from  
 2.0 microgram of total RNA, treated with T4 DNA polymerase  
 and purified by ethanol-precipitation. The cDNAs were  
 ligated to lone-linker lI-SalI, purified by  
 phenol/chloroform, and separated from free linkers by  
 Centricon 100. Then, the cDNAs were amplified by  
 long-range high fidelity PCR using Ex Tag polymerase  
 (Takara) with a primer SalI-S. The products were purified  
 by phenol/chloroform and Centricon 100. The cDNAs were  
 digested with SalI and NotI enzymes and cloned into  
 SalI/NotI site of pSPORT1 plasmid vector. The DH10B E.  
 coli host was transformed with the ligation mixture by the  
 standard chemical method. The average insert size is about  
 3.2 Kb. The library was constructed by Julian Piao."

BASE COUNT

134 a 172 c 154 g 133 t

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 Pred. No.: 2,02e-94 Length: 593  
 Score: 1016.00 Matches: 195  
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 Best Local Similarity: 99.49% Mismatches: 0  
 Query Match: 29.48% Indels: 0  
 DB: 14 Gaps: 0

US-09-991-053-10 (1-653) x CA890729 (1-593)

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Search completed: January 23, 2004, 01:40:43  
 Job time : 3633 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 22, 2004, 16:52:22 ; Search time 139 Seconds  
(without alignments)  
7433.654 Million cell updates/sec

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Perfect score: 2341  
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Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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1	2171.8	92.8	2185	US-09-996-243-728	Sequence 228, App
2	605	25.8	2906	US-09-996-243-500	Sequence 500, App
3	439.8	18.8	972	US-09-482-273-13	Sequence 13, Appl
4	430	18.4	984	US-09-482-273-82	Sequence 82, Appl
5	108.8	4.6	2019	US-09-063-950-3	Sequence 3, Appl
6	108.8	4.6	2768	US-09-996-243-51	Sequence 51, Appl
7	108.8	4.6	2852	US-09-063-950-1	Sequence 1, Appl
8	85.4	3.6	1685	5340934-1	Patent No. 5340934
9	80.6	3.4	2724	US-09-170-496D-263	Sequence 263, App
10	80.6	3.4	2724	US-09-170-496D-277	Sequence 277, App
11	77	3.3	4843	US-08-986-485-1	Sequence 1, Appl
12	75.8	3.2	5176	US-09-182-024A-1	Sequence 1, Appl
13	71.8	3.1	2818	US-09-620-312D-92	Sequence 92, Appl
14	71.2	3.0	1777	US-09-461-325-40	Sequence 40, Appl
15	66.8	2.9	7452	US-08-592-500-1	Sequence 1, Appl
16	66.8	2.9	7452	US-08-195-006-1	Sequence 1, Appl
17	66.8	2.9	7452	BCT-US94-0744A-1	Sequence 1, Appl
18	66.2	2.8	4104	US-09-996-243-277	Sequence 277, App
19	63.6	2.7	8378	PCT-US91-09055-1	Sequence 1, Appl
20	62	2.6	3747	US-10-042-810-1	Sequence 1, Appl
21	62	2.6	3837	US-10-042-810-3	Sequence 3, Appl
22	62	2.6	4068	US-10-042-810-5	Sequence 5, Appl
23	56	2.4	3083	US-09-484-970B-169	Sequence 169, App
24	52.8	2.3	6814	US-09-484-970B-66	Sequence 66, Appl
25	50	2.1	50	US-09-996-243-251	Sequence 251, App
26	49.8	2.1	2159	US-08-286-870A-7	Sequence 7, Appl
27	49.6	2.1	2082	US-08-985-335-4	Sequence 4, Appl

28	49.6	2.1	2082	US-09-410-372-4	Sequence 4, Appl
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34	48.2	2.1	1600	US-08-254-359A-12	Sequence 12, Appl
35	48.2	2.1	1600	US-08-483-043-12	Sequence 12, Appl
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## ALIGNMENTS

RESULT 1  
US-09-996-243-228  
Sequence 228, Application US/09996243  
Patent No. 6478825  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Goddard, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: KJavain, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC3  
CURRENT APPLICATION NUMBER: US/09/996,243  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28

[illegible]

PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 92.8%; Score 2171.8; DB 4; Length 2185;  
Best Local Similarity 99.7%; Pred. No. 0;  
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QY 1179 ATTCACTGCTGTGGCGGCTGTGATCTTCCATGACATGCAAGGCGGTACTGCTGG 1238  
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QY 1659 GTTACCAAGCGGAGTATACCACTCTTACCAAGGCTGCTCATTCAGACTAACCCGTGTGCCA 1718  
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QY 1899 CCGCGCGGACTGTTGAGTATATCCAGGTGAGCAAGACATCCGAGCAACATCCGAG 1958  
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Db      2161 AATTTAAGACAAAGTCAAA      2183

RESULT 2
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; Patent No. 6478825
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyere, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltzen, Mary E.
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; APPLICANT: Godowski, Paul J.
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C13
; CURRENT APPLICATION NUMBER: US/09/996,243
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
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; PRIOR APPLICATION NUMBER: 60/088861
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; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
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; PRIOR FILING DATE: 1998-06-16
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; PRIOR FILING DATE: 1998-06-18
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; PRIOR FILING DATE: 1998-06-18
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 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091978  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Query Match 25.8%; Score 605; DB 4; Length 2906;  
 Best Local Similarity 61.8%; Pred. No. 2,1e-151;

Matches 1000; Conservative 0; Mismatches 610; Indels 9; Gaps 2;  
 QY 339 GGCCCCAGAACTGCCCCCTGCTGCTCGGCAAGTAAACGATTGAGAAAGTGTGCA 398  
 Db 939 GGGCTCAGACCTGCCCCCTTGTGTGTCTTGCAGCAACGATTGAGAAAGTGTG 998  
 QY 399 CGGCGCGGGGCTCTCCGAGGTTCCCGAGGGATTCCCTCGAAACACCGGTACTCAACC 458  
 Db 999 TTGGGAAAAACCTGCGTAGGTTCCGATGGCATCTCCACCAACACGCTGTGAAC 1058  
 QY 459 TCATGGAACAACATCCAGATATCCAGGCCAACCTTCGCGACCTCCACCCTGG 518  
 Db 1059 TCCATGGAACAACATCCAGATATCCAGGCCAACCTTCGCGACCTCCACCCTGG 1118  
 QY 519 AGGTCCTGCAAGTGGGAGAACTCCATCCGAGATGAGAGTGGGGCTTCAACGGCC 578  
 Db 1119 AATCTTCAAGTGGAGGAAACCATATGAAACATTAATTTGGGGCTTCAATGTC 1178  
 QY 579 TGCGCAGCTCAGACACCTGAGCTGTCGACAACTGGCTGACAGTATCCTAGCGGG 638  
 Db 1179 TGGGAACTCACAACCTGGAACCTTTGACAAATGCTTTACTACATCCCAATGAG 1238  
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 Db 1239 CTTTGTATCTTGTCTAACTGAAGAGCTGTGGTGGCAACACCCCATGGAAGA 1298  
 QY 699 TCCCTCTTACGCTTCAACCGGGTCCCTCATGGCCCTGAGATTGGGGAGCTCA 758  
 Db 1299 TCCCTCTTATGCTTTTAAACGAATTCCTTTGGCGCGCATGAGATTGGGGAAATGA 1358  
 QY 759 AGAAGCTGAGATATCTGAGGAGCTTTGAGGGGCTGTCAACCTCAAGATCTGA 818  
 Db 1359 AAGACTTTATATCATCTCAAGAGGCTTTGAGGCTGTCTCAACTTGAAGTATTTGA 1418  
 QY 819 ACTTGGCATGTGCAACATTAAAGACATGCCAATCTACCCCTGTGGGGCTGAGG 878  
 Db 1419 ACCTTGCATGTGCAACCTTCGGGAATCCCTTAACCTCACACCGCTCATTAAGTATG 1478  
 QY 879 AGCTGAGATGTCAAGGAACCACTTCCCTGAGATCAGGCTGGCTCTTCAATGGCTGA 938  
 Db 1479 AGCTGATCTTCTGGGAATCATTTATCTCCATCAGGCTGGCTCTTCAAGGTTTGA 1538  
 QY 939 GCTCCCTCAAGAAAGCTGGGTATGAACTCACAGGCTACGATTTAGAGGGAATGCTT 998  
 Db 1539 TGCACCTTCAAAAACGTGTGATGATGATCCAGATTTCAAGTATGAAAGGAATGCTT 1598  
 QY 999 TTGACGGGCTGGCTTCACTTGTGGAATCACTTGGCCCAATTAACCTCTCTTGGC 1058  
 Db 1599 TTGACAACTTCAAGTACTAGTGAAGATCAACCTGGACACAAATTAATTAATGTC 1658  
 QY 1059 CCCATGACCTTTTACCCCGCTGAGTACTGTGTGATGATCTTACACCAACCTTT 1118  
 Db 1659 CTCATGACCTTCTACCTCCCTTGATCATCTAGAGCGGAATTAATTAATTAATTAAT 1178  
 QY 1119 GGAACGTGATTTGATGATCTGTGGCTAGCTGTGGCTTTCAGATATATATCCCA 1178  
 Db 1719 GGAACGTGATTTGATGATCTGTGGCTAGCTGTGGCTTTCAGATATATATATCCCA 1778  
 QY 1179 ATTCCACTGTGTGGCGCTGTATGCTCCATGACATGCGAGGCGGTACTCTGTGG 1238  
 Db 1779 AACAGCTTGTGTGGCGGTGTATGACCTCTCCCAATCTAAAGGGAGGTATCTGTGG 1838  
 QY 1239 AGGTGACCAAGGCTCTTCAAGTGTGCTGCCCCCTTCAATGAGACGACCTGAGACC 1298  
 Db 1839 AGCTGACCAAGATTAATTAATGATGATCTCGGAGATTGAGAGCCCTGACAGACC 1898  
 QY 1299 TCAACATTTCTGAGGGGTGAGTGGAGAACTTAAGTGTGGAATCCCTCTATGTCCT 1355  
 Db 1899 TCAATGTCACTGAGGAGTGGAGCTGAGTGAATGTGGAGCTTCAATTCCTGAT 1958  
 QY 1356 CCGTGAAGTGTGTGCTGCTCAATGAGACAGTGTCAAGCCAGCTCCCGACCAAGGA 1415  
 Db 1959 CTGATCTTGTGATTAATCTCAAAATGGAACATGATGACATGAGGGGCTTAAGTGTGGA 2018

QY 1416 TCCTGCTCTCAACGACGCGACCTTGAACCTTTCCACGTCGCTTTCAGACACTGCGG 1475  
DB 2019 TAGCTGCTCAGATGATGATGATGATTAATTTTCAAAATGTAATGTCAGATACAGGCA 2078  
QY 1476 TGTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1535  
DB 2079 TGTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2138  
QY 1536 GGACGACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1595  
DB 2139 TTA-----CTGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 2192  
QY 1596 CCACGAGATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1655  
DB 2193 CTATGAAACGCTCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2252  
QY 1656 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1715  
DB 2253 TGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2312  
QY 1716 CCAAGCAGTGGGACGATGATGATGATGATGATGATGATGATGATGATGATGATG 1775  
DB 2313 CAGAGAAACCTTCAACGATGATGATGATGATGATGATGATGATGATGATGATGATG 2372  
QY 1776 AAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1835  
DB 2373 AGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2432  
QY 1836 CCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1895  
DB 2433 CAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2492  
QY 1896 CAGCGCGCGGACGATGATGATGATGATGATGATGATGATGATGATGATGATG 1954  
DB 2493 CCCCAACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2551

RESULT 3  
US-09-482-273-13  
; Sequence 13, Application US/09482273  
; Patent No. 6534631  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 71 Human Secreted Proteins  
; FILE REFERENCE: P2030P1  
; CURRENT APPLICATION NUMBER: US/09/482,273  
; EARLIER FILING DATE: 2000-01-13  
; EARLIER APPLICATION NUMBER: PCT/US99/15849  
; EARLIER FILING DATE: 1999-07-14  
; EARLIER APPLICATION NUMBER: 60/092,921  
; EARLIER FILING DATE: 1998-07-15  
; EARLIER APPLICATION NUMBER: 60/092,922  
; EARLIER FILING DATE: 1998-07-15  
; EARLIER APPLICATION NUMBER: 60/092,956  
; NUMBER OF SEQ ID NOS: 267  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 973  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-482-273-13

Query Match 18.8%; Score 439.8; DB 4; Length 973;  
Best Local Similarity 73.5%; Pred. No. 1.4e-107;  
Matches 561; Conservative 0; Mismatches 202; Indels 0; Gaps 0;  
QY 319 CGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 378  
DB 205 CGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 264  
QY 379 GTTACGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 438

DB 265 GGCCAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 324  
QY 439 GAACACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 498  
DB 325 CAACACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 384  
QY 499 CCGGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 558  
DB 385 CAACGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 444  
QY 559 GGTGGGGGCTTCAACGCGCTGATGATGATGATGATGATGATGATGATGATGATGATG 618  
DB 445 GGTGGGGGCTTCAACGCGCTGATGATGATGATGATGATGATGATGATGATGATGATG 504  
QY 619 GACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 678  
DB 505 GACCAAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 564  
QY 679 CAACACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 738  
DB 565 GAACACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 624  
QY 739 CTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 798  
DB 625 CTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 684  
QY 799 GTTCAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 858  
DB 685 GGTCAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 744  
QY 859 CCCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 918  
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DB 805 GGGCTCTCTTCAACGCGCTGATGATGATGATGATGATGATGATGATGATGATGATG 864  
QY 979 CTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1038  
DB 865 CACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 924  
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RESULT 4  
US-09-482-273-82  
; Sequence 82, Application US/09482273  
; Patent No. 6534631  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 71 Human Secreted Proteins  
; FILE REFERENCE: P2030P1  
; CURRENT APPLICATION NUMBER: US/09/482,273  
; EARLIER FILING DATE: 2000-01-13  
; EARLIER APPLICATION NUMBER: PCT/US99/15849  
; EARLIER FILING DATE: 1999-07-14  
; EARLIER APPLICATION NUMBER: 60/092,921  
; EARLIER FILING DATE: 1998-07-15  
; EARLIER APPLICATION NUMBER: 60/092,922  
; EARLIER FILING DATE: 1998-07-15  
; EARLIER APPLICATION NUMBER: 60/092,956  
; NUMBER OF SEQ ID NOS: 267  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 82  
; LENGTH: 984  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-482-273-82





;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730P1C13  
;; FILE REFERENCE: P2730P1C13  
;; CURRENT APPLICATION NUMBER: US/09/996,243  
;; CURRENT FILING DATE: 2001-11-14  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/065186  
;; PRIOR FILING DATE: 1997-11-12  
;; PRIOR APPLICATION NUMBER: 60/065311  
;; PRIOR FILING DATE: 1997-11-13  
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;; PRIOR FILING DATE: 1997-11-24  
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;; PRIOR FILING DATE: 1998-02-25  
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;; PRIOR APPLICATION NUMBER: 60/083322  
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 ; PRIOR FILING DATE: 1998-07-02  
 ; PRIOR APPLICATION NUMBER: 60/091633  
 ; PRIOR FILING DATE: 1998-07-02  
 ; PRIOR APPLICATION NUMBER: 60/091978  
 ; PRIOR FILING DATE: 1998-07-07  
 ; PRIOR APPLICATION NUMBER: 60/091982  
 ; PRIOR FILING DATE: 1998-07-07  
 ; PRIOR APPLICATION NUMBER: 60/092182  
 ; PRIOR FILING DATE: 1998-07-09

Query Match 4.6%; Score 108.8; DB 4; Length 2768;  
 Best Local Similarity 54.9%; Pred. No. 5.2e-19;  
 Matches 237; Conservative 0; Mismatches 192; Indels 3; Gaps 1;

QY 336 CCGGGCCCCAGAACTGCGCCCTCGCTGCTGCAAGTAACAGATTGAGAGTGTGT 395  
 DB 175 CTGGGGTGAGAGGGGCTGCGATCCGGCTGCGAGTGCAAG--CCAGCCACAGACAGTCTTCT 221  
 QY 396 GCACGGCGCCGGGGCTCTCCGAGGTCGCGAGGGTATTCCTCGAACAACCCGGTACTCA 455  
 DB 232 GCACGTGCGCGCCAGGGGACACAGGTGCTCCGAGACGTGCCAACCCGACCGGTGGGGCTGT 221  
 QY 456 ACCTCATGAGAAACAATCATCAATGATCCAGGGCCGACACCTTCGCGACCTCCACCAACC 515  
 DB 292 ACCTCTTTGAGAACGCGCATCAACATGCTCGACGAGCAGCTTTCGCGGCTCGCGGGCC 351  
 QY 516 TGAAGGCTCGAGTGGGGAGAACTCCATCCGCGAGATTGAGTGGGGGCTTCAAGC 575  
 DB 352 TGAAGCTCTGAGCTGTCAAGAACCAATCGCAGCTGCCAGCGGGGTCTTCCAGC 411  
 QY 576 GCCTGGCCAGCCTCAGCAACCTGGAGCTGTTCGACAAGTGAAGTATCCCTAGCG 635  
 DB 412 CACTCGGCAACTCAGAACCTGAGCTTGAAGCGGCAACAGGCTGATGAATCACAATG 471  
 QY 636 GGGCTTTGAATACTGTGCAAGCTGGGAGCTGTGCTTGCACAAACCCCATCGAAA 695  
 DB 472 AGACCTTCGAGCTGCGCGGCTCGAGCGCTCTTACCTGAGGGAAGAACCGATCCGCC 531  
 QY 696 GCATCCCTTTAGAGCTTCAACCGGGTGCCTCCCTCAAGCGCTTGAAGTGGAGGAGC 755  
 DB 532 ACATTCAGCGCTGTGCTTCAAGCAGCTCGACCGCTCTGAGAGCTCAAGCTGAGAGCA 591  
 QY 756 TCAAGAGCTGG 767  
 DB 592 ACAGCTGCGGG 603

RESULT 7  
 US-09-063-950-1  
 ; Sequence 1, Application US/09063950C  
 ; Patent No. 6225085  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Holtzman, Douglas A.  
 ; TITLE OF INVENTION: NOVEL LSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES  
 ; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: MEI-019  
 ; CURRENT APPLICATION NUMBER: US/09/063,950C  
 ; CURRENT FILING DATE: 1998-04-21  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1  
 ; LENGTH: 2852  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (160)..(2178)  
 US-09-063-950-1

Query Match 4.6%; Score 108.8; DB 3; Length 2852;  
 Best Local Similarity 54.9%; Pred. No. 5.3e-19;  
 Matches 237; Conservative 0; Mismatches 192; Indels 3; Gaps 1;

QY 336 CCGGGCCCCAGAACTGCGCCCTCGCTGCTGCAAGTAACAGATTGAGAGTGTGT 395  
 DB 215 CTGGGGTGAGAGGGGCTGCGATCCGGCTGCGAGTGCAAG--CCAGCCACAGACAGTCTTCT 271  
 QY 396 GCACGGCGCCGGGGCTCTCCGAGGTCGCGAGGGTATTCCTCGAACAACCCGGTACTCA 455  
 DB 272 GCACGTGCGCGCCAGGGGACACAGGTGCTCCGAGACGTGCCAACCCGACCGGTGGGGCTGT 331  
 QY 456 ACCTCATGAGAAACAATCATCAATGATCCAGGGCCGACACCTTCGCGACCTCCACCAACC 515  
 DB 332 ACCTCTTTGAGAACGCGCATCAACATGCTCGACGAGCAGCTTTCGCGGCTCGCGGGCC 391  
 QY 516 TGAAGGCTCGAGTGGGGAGAACTCCATCCGAGATTGAGTGGGGGCTTCAAGC 575  
 DB 392 TGAAGCTCTGAGACCTGTCAAGAACCAATGCGCAGCTGCCAGCGGGTCTTCCAGC 451  
 QY 452 CACTCGGCAACTCAGAACCTGAGCTTGAAGCGGCAACAGGCTGATGAATCACAATG 511  
 DB 636 GGGCTTTGAATCTGTCCAAAGCTGCGGAGCTGTGCTTGCACAAACCCCATGAAA 695  
 QY 512 AGACCTTCGAGCTGCGCGGCTCGAGCGCTCTTACCTGAGGGAAGAACCGATCCGCC 571  
 DB 696 GCATCCCTTTAGAGCTTCAACCGGGTGCCTCCCTCAAGCGCTTGAAGTGGAGGAGC 755  
 DB 572 ACATTCAGCGCTGTGCTTCAAGCAGCTCGACCGCTCTTGAAGCTCAAGCTGAGAGCA 631  
 QY 756 TCAAGAGCTGG 767  
 DB 632 ACAGCTGCGGG 643

RESULT 8  
 5340934-1  
 ; Patent No. 5340934  
 ; APPLICANT: TERMINE, JOHN D.; YOUNG, MARIAN F.; FISHER, LARRY W.  
 ; ROBEY, PAMELA G.  
 ; TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS  
 ; NUMBER OF SEQUENCES: 13  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/432,044  
 ; FILING DATE: 03-NOV-1989  
 ; SEQ ID NO:1:  
 ; LENGTH: 1685  
 5340934-1

Query Match 3.6%; Score 85.4; DB 6; Length 1685;  
 Best Local Similarity 46.8%; Pred. No. 7.1e-13;  
 Matches 346; Conservative 0; Mismatches 381; Indels 12; Gaps 2;

QY 376 CCAATTCAAGCAAGTGTGTGACGCGCGGGGCTCTCCGAGTCCCGAGGATATTC 435  
 DB 327 CCACTGCGGGGTGTTCAGTGTCCGACCTGGGTGGAAGTGTGTGCCCAAGAGATCTC 386

```

Qy 436 CTGGAACCCGGTACTCAACTTCATGAGAACAAATCCAGATGATCCAGGCCGAC 495
Db 387 CCTGACACCAAGCTGTGAGCTGACAGAACAAAGACATCTCCAGGCTCCGACAGATGA 446
Qy 496 CTTCCGCACTTCCACCACTTGAAGTCTGACATTTGGGACAGAACTCCATCCGCGAT 555
Db 447 CTTCAAGGGTCTCCAGCACTCTACGCTCTGTGTGTGAACAACAAGATCTCAAGAT 506
Qy 556 TGAAGTGGGAGCTTCAACGAGCTGGCAGGCTTCAGACCTCGAGCTGTTCGAACTG 615
Db 507 CCAATGAAAGGCTTTCAGCCCACTGCGGAGCTGAGAGATCTACATCTCAAGAACCA 566
Qy 616 GCTGACATCATCTTCAGCGGGCTTTGAATACCTGTTCAGCTGCGGAGCTGTGCT 675
Db 567 CCTGGTGAAGATCCGCCCC-----ACCTAACCCAGCTCCCTGGTGAAGCTCCGAT 617
Qy 676 TCGCAACAAACCCATTCGAAAGATTCCTCTTAAGCCTTCAACGGGGTCCCTCCAT 735
Db 618 CCACGACAAACCGCATCCGCAAGGTGCCAAGGAGTGTTCAGCGGGCTCCGAAATGAA 677
Qy 736 GCGCTGGAATTTGGGGAGCTCAAGAACTGGAATATCTCTGAGGAGCTTTTGAAGG 795
Db 678 CTGATCGAGATGGGCGGGAACCCACTGGAAGACAGTGGCTTTGAAGCTGAGCCTTGA 737
Qy 796 GCTGTTCAACCTCAAGTATCTGAACTTGGGCAATGCAACATTAAGAATGCCCAATCT 855
Db 738 TGGCTGAAGCTCAACTACTGCGCATCTCAGAGGCCAAGCTGACTGCGCATCCCAA--- 794
Qy 856 CACCCCTGTGGGCTGGAAGAGCTGGAATGTCAAGGAAACCACTTCCCTGAGATAG 915
Db 795 AGACCTCCCTGAGACCTGGAATGAATCACTCAACCAACAACAAATCCAGGCGCATGA 854
Qy 916 GCCTGCTCTCTTCATGAGCTGAGTCCCTCAAGAAAGCTTGGGTCATGAATCAAGT 975
Db 855 ACTGAGAGACCTGCTTCCGCTACTCCAAGCTGACAGGCTGGGCTTGAAGCCACACAGAT 914
Qy 976 CAGCTGATGAGCGGAATGCTTTTGAAGCGGCTGAGCTTCACTTGTGAATCAACTTGGC 1035
Db 915 CAGATGATCGAAGACGGGAGCTTGAAGCTTCTGCGCAACCTCCGAGGACTCCACTTGA 974
Qy 1036 CCAATTAACCTCTTCTTTTGGCCCAAGACTCTTTTACCCGCTGAGTACTGTGTGA 1095
Db 975 CAACAACAAAGTTGGCAGGCTGCTCAGGGCTCCAGACCTCAAGCTCTCCAGTGTGT 1034
Qy 1096 GTTGACATCAACACACAC 1114
Db 1035 CTATCTGCACTCCAAACAC 1053

```

## RESULT 9

```

US-09-170-496D-263
; Sequence 263, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 263
; LENGTH: 2724
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-263

```

Query Match 3.4%; Score 80.6; DB 4; Length 2724;  
 Best Local Similarity 49.7%; Pred. No. 1,7e-11;  
 Matches 234; Conservative 0; Mismatches 234; Indels 3; Gaps 1;

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Qy 379 GTTCAGCAAGTGTGTGACAGCGCGGGGCTTCTCCAGAGTCCGACAGGATTCCTTC 438
Db 138 GTTGCTCAGGGTGTGAGTGTCTCCAGCTGGGGCTCTCGAGCTCCTTCCAACTCAGCT 197
Qy 439 GAACACCCGGTACTCAACTCATGAGAACAAACATTCAGATATCCAGGCCACACTT 498
Db 198 CTTCACTCTTACTTGAACCTCAGTATGAAACAAATCAGTCACTGTCTCCGAATCCCT 257
Qy 499 CCGCACTTCACACACCTGAGAGTCCGAGTGGGAGGAACTCCATCCGAGATTGA 558
Db 258 GCCAGTCTCCGCTTCTTGAAGAGTATCCTTTGCGGGAAGCTTGTGACATATTC 317
Qy 559 GATGGGGCTTCAACGCGCTGCGACCTCAGACACCTTGAAGCTTGTGACAACTGGCT 618
Db 318 CAAGGAGATTCATCTGCGCTTTAAGTCTTAAAGTCTTATCTGAGATATACGT 377
Qy 619 GACAGTATCTCTACGCGGGCTTTGAATATCTGTCCAGCTGCGGAGCTGTGCTTG 678
Db 378 AAGACAGTACCCACAGAACCTCTGCAAAATTTGCGAAGCTTCAATCCCTGCTTGA 437
Qy 679 CAACACCCGATGAAAGCATCCCTCTTACGCTTCAACCGGGTCCCTCCATAGC 738
Db 438 TGCTAACCAATCAGCTATGTGCTCCAGCTGTTTCAAGGCTGATTCCTTGAAGCA 497
Qy 739 CTTGACTTGGGAGCTCAAGAACTGAGTATCTCTGAGGAGCTTTTGAAGGCT 798
Db 498 CTTG---TGGCTGATATGAAATGCTTTAACAAGATCCCGCTCAGGCTTTTGAAGTTT 554
Qy 799 GTTCAACCTCAAGTATCTGAACTTGGGAGTGTGCAACATTAAGAATGCTC 849
Db 555 ATCGCATTCACAGCATGATGAGCTTGGCTTGAACAAATACACACATACC 605

```

## RESULT 10

```

US-09-170-496D-277
; Sequence 277, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 277
; LENGTH: 2724
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-277

```

Query Match 3.4%; Score 80.6; DB 4; Length 2724;  
 Best Local Similarity 49.7%; Pred. No. 1,7e-11;  
 Matches 234; Conservative 0; Mismatches 234; Indels 3; Gaps 1;

```

Qy 379 GTTCAGCAAGTGTGTGACAGCGCGGGGCTTCTCCAGAGTCCGACAGGATTCCTTC 438
Db 138 GTTGCTCAGGGTGTGAGTGTCTCCAGCTGGGGCTCTCGAGCTCCTTCCAACTCAGCT 197
Qy 439 GAACACCCGGTACTCAACTCATGAGAACAAACATTCAGATATCCAGGCCACACTT 498
Db 198 CTTCACTCTTACTTGAACCTCAGTATGAAACAAATCAGTCACTGTCTCCGAATCCCT 257
Qy 499 CCGCACTTCACACACCTGAGAGTCCGAGTGGGAGGAACTCCATCCGAGATTGA 558
Db 258 GCCAGTCTCCGCTTCTTGAAGAGTATCCTTTGCGGGAAGCTTGTGACATATTC 317
Qy 559 GATGGGGCTTCAACGCGCTGCGACCTCAGACACCTTGAAGCTTGTGACAACTGGCT 618

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Db 318 CAAGGAGCATTCAGTCCCTTTACAGTCTTAAAGTTCTTATGCTGCAAGATAATCAGCT 377  
Qy 619 GACAGTCATCCCTAGCGGGGCTTTTGAATACCTGTCACAGCTGCGGAGCTGTGCTCG 678  
Db 378 AGACACGTAACCAAGAGCTCTGCAAGATTGCGAAGCTTCAATCCCTGCTGGA 437  
Qy 679 CAACAACCCATCGAAGATCCCTTTACGCTTCAACCGGGTCCCTCCCTCATGCG 738  
Db 438 TGTAAACCATCAGTATGTCGCCCAAGCTGTTCAGTGGCTGCATTCCTGAGGCA 497  
Qy 739 CTTGAGCTGGGGAGCTCAAGAGCTGAGTATCTCTGAGGAGCTTTGAGGGGCT 798  
Db 498 CCG---TGGCTGAGAGCAATCGTTAACAGAAATCCCGTCCAGCTTTTGAAGTTT 554  
Qy 799 GTTCAACCTCAAGTATCTGAATTTGGGCAATGTCACATTAAGAATGCGC 849  
Db 555 ATCGGATTCAGACCATGACTTGGCCCTGGAACAAATACCAATAC 605

## RESULT 11

US-08-986-485-1  
; Sequence 1, Application US/08986485  
; Patent No. 6046030  
; GENERAL INFORMATION:  
; APPLICANT: WU, SHUJIAN  
; APPLICANT: SWEET, RAYMOND  
; APPLICANT: TRUNEH, ALEMSEGED  
; TITLE OF INVENTION: A HUMAN LIG-1 HOMOLOG (HLIG-1)  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: RATNER & PRESTIA  
; STREET: P.O. BOX 980  
; CITY: VALLEY FORGE  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19482  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/986,485  
; FILING DATE: 08-DEC-1997  
; CLASSIFICATION:  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 60/059,448  
; FILING DATE: 22-SEP-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PRESTIA, PAUL F  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: GH-70264  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-407-0700  
; TELEFAX: 610-407-0701  
; TELEX: 846169  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4843 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; US-08-986-485-1

Query Match 3.3%; Score 77; DB 3; Length 4843;  
Best Local Similarity 55.4%; Pred. No. 2.1e-10;  
Matches 149; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

Qy 450 ACCTCAACCTCATGAGAAACAATCCAGATGATCCAGGCCGACACCTTCCGCACTCC 509  
Db 689 AACTGACCTCATCGGACAGATTCGCTGATAGAGGGCTCACCTTCAGGAGGCTCA 748

Qy 510 ACCACCTGAGGTCCTGCAAGTTGGGCAAGAACTCATCCGAGATTGAGTGGGGCT 569  
Db 749 ACAGCTTGAGGTCGTGAAGCTTACAGCAAAACATTCAGAAATGACAGATGAGGGCT 808  
Qy 570 TCAAGGCTTGGCCAGACCTCAGACCTTGAAGCTGTTCACAACATGAGTATCC 629  
Db 809 TCTGGGAGCTGTCAAAATGATGCTGACACTGAGTACAGACACCTGATGAGATGA 868  
Qy 630 CTAGCGGGGCTTTGAATACCTGTCACAGCTCGGGAGCTGTGGCTTGGCAACACCA 689  
Db 869 AAGGAGCTGCTCTAGAGGCTTCAGGCTTCAGGCTTCAGGCTTCAGGCTTCAGGCT 928  
Qy 690 TCGAAGCATCCCTCTTACGCTTCAAC 718  
Db 929 TCGCTGATTCACCGCAAGGCTGGAGC 957

## RESULT 12

US-09-182-024A-1  
; Sequence 1, Application US/09182024A  
; Patent No. 6342370  
; GENERAL INFORMATION:  
; APPLICANT: Connolly, Timothy  
; APPLICANT: Rajput, Bhanu  
; TITLE OF INVENTION: Human Silt Polypeptide and Polynucleotides Encoding  
; FILE REFERENCE: 640100-271  
; CURRENT APPLICATION NUMBER: US/09/182,024A  
; PRIOR FILING DATE: 1998-10-29  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/096,420  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 5176  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURES:  
; OTHER INFORMATION: Description of Artificial Sequence: cDNA coding for  
; OTHER INFORMATION: the human silt polypeptide of SEQ ID NO:2  
US-09-182-024A-1

Query Match 3.2%; Score 75.8; DB 4; Length 5176;  
Best Local Similarity 48.1%; Pred. No. 4.6e-10;  
Matches 246; Conservative 0; Mismatches 262; Indels 3; Gaps 1;

Qy 338 GGGCCCCAGAACTGCCCCCTCGCTGCTGTCAGTAACAGTTTCAAGGAGTGTGC 397  
Db 301 GGGCTTCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360  
Qy 398 ACGCGCGGGGCTCTCCAGAGTCCGCAAGGATTCCTCGAACAACCCGTAACCTCAAC 457  
Db 361 CAGCGGCTGGGCTCGCGCGGCTGCTCGGGGATCCCGAAGCTGAGGCGCTTGAC 420  
Qy 458 CTCATGAGAAACAATCTCAAGATTCAGAGCCGCAACCTTCCGCACTTCACCACTG 517  
Db 421 CTGAGACAAATATATTCACAGAGATCAACAGATGATGATGATGATGATGATGATG 480  
Qy 518 GAGGCTCTGAGTGGGAGGAACTCCATCCGAGATGAGGAGTGGGGCTTCAACGCG 577  
Db 481 CGAGCTTTCATGTAAGAAACAACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 540  
Qy 578 CTGGCCAGCTCAGCAACCTGAGCTGTTGCAACATGCTGACACTCAATCCCTAGCGG 637  
Db 541 CTGAACACAGTGAAGAGCTGCGCTGAACAAGATTAAGTCAAGTCAAGTCAAGTCA 600  
Qy 638 GCGTTGAATACCTGTCAGAGCTGCGGGAGCTGTGCTTGCACAACACCCATCGAAGC 697  
Db 601 CTTTTCAGAGCAAGCGGAGCTCAACAGATTAAGTTTGAAGAAAACCAAGATTCAGG 660  
Qy 698 ATCCCTCTTAAAGCTTCAACCGGGTGCCTCCTCATGCGGCTGAGATTGGGGAGCTC 757

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Db      661 ATCCGAGGAAGGCTCCCGGATACCCGATGTGAAGAACTGCAACT---GGAACAAC 717
Qy      758 AAGAGCTGAGATATATCTGTGAGGGAGCTTTGAGGGGCTTTCAACCTCAAGTATCTG 817
Db      718 AACCACTACAGCTGCTGATTTGAAGATGAGGCTTCGAGCGCTGGCGCATTTGAGATCTTT 777
Qy      818 AACTGGGCACTGTGCAACATTAAAGACATGC 848
Db      778 ACCCTCAACAACAACAACATCATGTCGATCC 808

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## RESULT 13

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US-09-620-312D-92
; Sequence 92, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyun
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aifeng J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/620,312D
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc_fl_genes Version 1.0
; SEQ ID NO 92
; LENGTH: 2818
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (449)..(2818)
US-09-620-312D-92

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Query Match 3.1%; Score 71.8; DB 4; Length 2818;  
 Best Local Similarity 50.3%; Pred. No. 3.9e-09;  
 Matches 231; Conservative 0; Mismatches 222; Indels 6; Gaps 2;

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Qy      448 GTACCTACCTCATGGAACAACATCCAGATGATCCAGCCGACACTTCGCCACCT 507
Db      685 GGAACCTGACCTGTCCGAGAAACATCAACATCCAGCCCTTTTCTTCTGAGACT 744
Qy      508 CCACCACTGAGAGTCTGTGAGTTGGGAGAACTCCATCCGAGATTAGGTGGGGG 567
Db      745 GGAAGCTCTCGCTCCCTGATCTTGACAGCAATCGGCTCCCAAGCTTGGGAGGAC 804
Qy      568 CTTCACGCGCTGCGCAGCTTCAGACCTTGAGCTTTGCAACTGGCTGACAGTCAT 627
Db      805 CTCCTCGGGGCTGTGCTCACTGCAAGCACTTATGCTGAACAACAACAGCTGGGGCAT 864
Qy      628 CCTAGCGGGGCTTT--GAATACCTGTCCAACTGCGGAGCTTGCTGGCTTGGCAA 664
Db      865 CGAGATGAGGCTTTGAGGACTTCTGCTGACATGAGAGATCTGACCTCTCTCAAA 924

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Qy      685 CCCCATGGAAGATCCCTCTTACGCTTCAACCGGGTGCCCTCCCTCATGCGCTGGA 744
Db      925 CAACCTTCATGGCTCTCCGTGGGACTCCGTGGAGGCAATGTCAACTCCACAGCTGAG 984
Qy      745 CTGGGGGAGCTCAGAACTGAGATATATCTGTAGGGAGCTTTTGGAGGGCTTTCAA 804
Db      985 CCT---GGAACAACCTCTGTATCATATCCGCGGACCTTTGGAGACTGACAGA 1041
Qy      805 CCTCAAGTATCTGAATCTGGGATGTGCAACATTAAAGCATGCCCATCTCACCCCT 864
Db      1042 ACTGGCCGCTGGATCTCACTCCATATGCGCTGCAGAACTGCCCCCTGATCCATCTT 1101
Qy      865 GGTGGGCTGAGGAGCTGAGATGTCAAGGAACCACTT 903
Db      1102 TGCCGCTCCAGAGGCTTGCGCTTGAACAACCACTT 1140

```

## RESULT 14

```

US-09-461-325-40
; Sequence 40, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruden et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; PRIOR FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 1777
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-325-40

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Query Match 3.0%; Score 71.2; DB 4; Length 1777;  
 Best Local Similarity 54.1%; Pred. No. 4.5e-09;  
 Matches 145; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

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Qy      474 TCCAGATGATCCAGGCGGACACCTTCGCGCACCTCCACCACTGAGAGTCTGCACTTG 533
Db      391 TCGGCTGTGAGACCTTGCAACATTCACGCGCTGGGCGGCTGACACAGGTGCACTTG 450
Qy      534 GGAAGATCTCATCCGCGAGATTGAGTGGGGGCTTCAACGCGCTGGCCAGCTCAGCA 593
Db      451 ACCGCTGCGGCTGCGAGAGCTGGGCGGCGCTGTTCCGCGGCTGGCTGCCTCAGT 510
Qy      594 CCTGAGAGCTGTTGCAACTGCTGCAAGTCAATCCCTAGCGGGGCTTTGAATACCTGT 653
Db      511 ACCTTACCTGCAAGCAACGCGCTGCAAGCACTGCTATATGACATCTTCGCACTTG 570
Qy      654 CCAAGCTGCGGAGCTCTGCTTTCGCAACAACCCATCGAAAGCATCCCTTCAAGCTT 713
Db      571 GCAACTTCAACAACCTCTTCTGCAAGGCAACCGCATCTCCAGCTGCCGAGCGGCT 630
Qy      714 TCAACGGGCTGCTTCCTCATGCGCTT 741
Db      631 TCGTGGGCTGCAACAGCTTCAGACCTCT 658

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RESULT 15  
US-08-592-500-1  
Sequence 1, Application US/08592500  
Patent No. 6005089  
GENERAL INFORMATION:  
APPLICANT: Lanza, Francois  
APPLICANT: Phillips, David R.  
APPLICANT: Cazenave, Jean-Pierre  
TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,500  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/089,455  
FILING DATE: 09-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Karen B.  
REGISTRATION NUMBER: 29,684  
REFERENCE/DOCKET NUMBER: 12418-28  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7452 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: intron  
LOCATION: 1462..2419  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2422..4101  
FEATURE:  
NAME/KEY: misc\_signal  
LOCATION: 68..76  
OTHER INFORMATION: /function= "Putlitive TPA responsive  
OTHER INFORMATION: element"  
OTHER INFORMATION: /label= TRE  
FEATURE:  
NAME/KEY: misc\_signal  
LOCATION: 471..478  
OTHER INFORMATION: /function= "Ets-1 cis-acting  
OTHER INFORMATION: sequence"  
OTHER INFORMATION: /label= Ets-1  
FEATURE:  
NAME/KEY: misc\_signal  
LOCATION: 493..502  
OTHER INFORMATION: /function= "Ets-1 cis-acting  
OTHER INFORMATION: sequence"  
OTHER INFORMATION: /label= Ets-1  
FEATURE:  
NAME/KEY: repeat\_region

LOCATION: 593..881  
OTHER INFORMATION: /rpt type= "other"  
OTHER INFORMATION: /label= Alu  
FEATURE:  
NAME/KEY: misc\_signal  
LOCATION: 897..904  
OTHER INFORMATION: /function= "Ets-1 cis-acting  
OTHER INFORMATION: sequence"  
OTHER INFORMATION: /label= Ets-1  
FEATURE:  
NAME/KEY: misc\_binding  
LOCATION: 1142..1149  
OTHER INFORMATION: /function= "Spi binding site"  
OTHER INFORMATION: /standard\_name= "Spi"  
FEATURE:  
NAME/KEY: misc\_signal  
LOCATION: 1178..1184  
OTHER INFORMATION: /function= "Ets-1 cis-acting  
OTHER INFORMATION: sequences"  
OTHER INFORMATION: /label= Ets-1  
FEATURE:  
NAME/KEY: TATA\_signal  
LOCATION: 1199..1203  
FEATURE:  
NAME/KEY: TATA\_signal  
LOCATION: 1263..1269  
FEATURE:  
NAME/KEY: misc\_binding  
LOCATION: 1285..1289  
OTHER INFORMATION: /function= "GATA-1 binding site"  
FEATURE:  
NAME/KEY: misc\_binding  
LOCATION: 1321..1326  
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Best Local Similarity 44.7%; Pred. No. 1.4e-07;  
Matches 352; Conservative 0; Mismatches 427; Indels 9; Gaps 2;

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QY 1049 TCTTCTTTGGCCCATGACTCTTAAACCGGCTGAGATCTGCTGAGAGTGTGATCTAC 1108
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Db 3244 GAGAAACC 3251
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Search completed: January 22, 2004, 22:07:18  
Job time : 145 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 22, 2004, 22:05:01 ; Search time 6570 Seconds  
(without alignments)  
4066.056 Million cell updates/sec

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Xgapop 10.0, Xgapext 0.5  
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Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2888711 seqs, 20454813386 residues  
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
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13: gb\_un.\*  
14: gb\_vl.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
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20: em\_om.\*  
21: em\_or.\*  
22: em\_ov.\*  
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24: em\_ph.\*  
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26: em\_ro.\*  
27: em\_sts.\*  
28: em\_un.\*

29: em\_vi.\*  
30: em\_hgt\_hum.\*  
31: em\_hgt\_inv.\*  
32: em\_hgt\_other.\*  
33: em\_hgt\_mus.\*  
34: em\_hgt\_pin.\*  
35: em\_hgt\_rtd.\*  
36: em\_hgt\_mam.\*  
37: em\_hgt\_vrt.\*  
38: em\_sy.\*  
39: em\_hgt\_hum.\*  
40: em\_hgt\_mus.\*  
41: em\_hgt\_other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3407	98.9	2185	6 AR252532	AR252532 Sequence
2	3407	98.9	2185	6 AX403341	AX403341 Sequence
3	3407	98.9	2185	6 AX464304	AX464304 Sequence
4	3407	98.9	3770	6 AF196976	AF196976 Homo sapi
5	3407	98.9	194043	2 AC116940	AC116940 Pan trogl
6	3407	98.9	197346	2 AC008039	AC008039 Homo sapi
7	3407	98.9	202911	2 AC119063	AC119063 Pan trogl
8	3400	98.7	171218	2 AC136196	AC136196 Papio anu
9	3400	98.7	176123	2 AC114887	AC114887 Papio anu
10	3374	97.2	2294	9 HSA297858	AJ297858 Homo sapi
11	3348.5	97.2	155852	2 AC135841	AC135841 Canis fam
12	3343.5	97.0	159915	2 AC137913	AC137913 Felis cat
13	3339.5	96.9	183761	2 AC136203	AC136203 Bos tauru
14	3339.5	96.9	199027	2 AC137061	AC137061 Bos tauru
15	3326	96.5	183772	2 AC138045	AC138045 Sus scrofa
16	3324.5	96.5	161980	2 AC115527	AC115527 Rattus no
17	3324.5	96.5	226981	2 AC127822	AC127822 Rattus no
18	3324.5	96.5	266789	2 AC131608	AC131608 Rattus no
19	3319.5	96.3	3188	10 AF290542	AF290542 Mus muscu
20	3319.5	96.3	161515	2 AC068662	AC068662 Mus muscu
21	3286.5	95.4	2202	10 AF300458	AF300458 Mus muscu
22	32197.5	63.8	104939	2 AC138556	AC138556 Takifugu
23	2197.5	63.8	131796	2 AC138558	AC138558 Takifugu
24	1898	55.1	2142	6 AX275019	AX275019 Sequence
25	1898	55.1	2397	6 AX392995	AX392995 Sequence
26	1898	55.1	2493	6 AX275017	AX275017 Sequence
27	1898	55.1	2756	6 AX590252	AX590252 Sequence
28	1898	55.1	3027	6 AX392983	AX392983 Sequence
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31	1832	53.2	2906	6 AX098385	AX098385 Sequence
32	1832	53.2	2906	6 AX403613	AX403613 Sequence
33	1832	53.2	2906	6 AX464234	AX464234 Sequence
34	1832	53.2	2906	6 AX697700	AX697700 Sequence
35	1832	53.2	2906	6 BD075607	BD075607 Secretory
36	1832	53.2	2906	6 BD172467	BD172467 Secreted
37	1832	53.2	2906	6 BD172786	BD172786 Secreted
38	1832	53.2	2906	6 BD173105	BD173105 Secreted
39	1832	53.2	2906	6 BD173424	BD173424 Secreted
40	1832	53.2	2906	6 BD175458	BD175458 Secretory
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RESULT 1

## ALIGNMENTS

AR252532 2185 bp DNA linear PAT 20-DEC-2002  
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 DEFINITION Sequence 228 from patent US 6478825.  
 AR252532  
 VERSION AR252532.1 GI:27300440  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 2185)  
 AUTHORS Winterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.  
 TITLE Implant, method of making same and use of the implant for the  
 treatment of bone defects  
 JOURNAL Patent: US 6478825-A 228 12-NOV-2002;  
 FEATURES Location/Qualifiers  
 source 1..2185  
 /organism="Unknown"  
 BASE COUNT 527 a 666 c 519 g 473 t  
 ORIGIN  
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 Percent Similarity: 99.39% Conservative: 1  
 Best Local Similarity: 99.23% Mismatches: 4  
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 Db 177 GCCGGGCCCCGAACTGCCCCCTCCGTTTCTGTCGTGACATACAGTTGAGCAAGGTGTG 236  
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 QY 81 AsnLeuMetGluAaAsnIleGlnMetIleGlnIaAspThrPheArgHisLeuHisHis 100  
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 QY 121 GlyLeuAlaSerLeuSerThrLeuGluLeuPheAspAsnTrpLeuThrValIleProSer 140  
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 Db 477 GGGGCTTTGAATCTGTCCAGCTGGGAGCTGGCTTCCCAACMACCCATCGAA 536  
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 Db 537 AGCATCCCCCTTTACGCTTCAACCGGGTGCCTCCCTCATAGCGCTGAGCTTGGGGAG 596  
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QY 221 GlnGluLeuGlnMetSerGlyAsnHisPheProGluIleArgProGlySerPheIleGly 240  
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 QY 261 AlaPheAspGlyLeuAlaSerLeuValGluLeuAsnLeuHisAsnAsnLeuSerSer 280  
 Db 837 GCTTTACGGGCTGGCTTCACTTGTGAACCTGACCTGGCCCAATTAACCTCTCTTCT 896  
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 QY 341 ValGluValAspGlnAlaSerPheGlnCySerAlaProPheIleMetAspAlaProArg 360  
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 QY 481 ThrGlyTyrGlnProAlaTyrThrThrSerThrValLeuIleGlnThrArgVal 500  
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 QY 501 ProIleGlnValAlaValProAlaThrAspThrThrAspLysMetGlnThrSerLeuAsp 520  
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OY		581	AlaalaatTrrAlaAlProSerGlyValSerGlyGluGlyAlaValAlaLeuProThr	600
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Db		1857	ATTTCATGACCATTAATTAACTAACACACTTAACAACGAGCACATGGGGCCACTGGACAGA	1911
OY		621	AenSerLeuGlyAenSerLeuHisProThrValThrThrIleSerGluProTyrllelle	640
Db		1917	AACGAGCCCTGGGGAATCTCTGGACCCCAAGTCACACACTATCTCGAACTTATAATT	1976
OY		641	GlnThrHisThrLysAspLysValGlnGluThrGlnIle	653
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DEFINITION	Sequence 228 from Patent WO0073454.			
ACCESSION	AK403341			
VERSION	AK403341.1	GI:21436886		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 Ashkenazi,A.D., Baker,K.P., Bobstein,D., Desnoyers,L., Eaton,D., Ferrara,N., Garber,H., Gerlitsen,G., Goddard,A., Godowski,P., Grimaldi,C.J., Gurney,A.L., Kijavyn,I., Napier,M.A., Pan,J., Paoletti,N.F., Roy,W., Stewart,T.A., Tamas,D., Watanabe,C.K., Williams,P., Wood,W.I. and Zhang,Z. Secreted and transmembrane polypeptides and nucleic acids encoding the same Patent: WO 0073454-A 228 07-DEC-2000;			
JOURNAL	Genentech Inc. (US)			
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Score:	3407.00	Matches:	648	
Percent Similarity:	99.39%	Conservative:	1	
Best Local Similarity:	99.23%	Mismatches:	4	
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DB:	6	Gaps:	0	
US-09-991-053-10 (1-653) x AX403341 (1-2185)				
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Db		117	TTCGTCACTTCACGCGCGCAATGTGGATTCTGTGTGCAGCCATGCTGCTCCGGCTTA	176
OY		41	AlaGlyProGlnAsnCysProSerValCysSerCysSerASngInpheSerLysValVal	60
Db		177	GCCGGGCCCCAGAACTGCCCTCCGTTCTGTGTGACGATACCACTTCAGCAAGGTGGTG	236
OY		61	CythrArGArgGlyLeusSerGluValProGlnglyIleProSerASnthrArgTyrlieu	80
Db		237	TGCACGCGCGCGGGGCTCTCCGAGGTCGCGCAGGGGTATTCCTCGAACAACCGGTACTTC	296
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RESULT 3  
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 DEFINITION Sequence 437 from Patent WO0140466.  
 ACCESSION AX464304  
 VERSION AX464304.1 GI:21899168  
 KEYWORDS  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
 AUTHORS Baker, K.P., Bereisni, M., Deforge, L., Desnoyers, L., Filvaroff, E.,  
 Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gunney, A.L.,  
 Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,  
 Wood, W.L. and Zhang, Z.  
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 Genentech Inc. (US)  
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VERSION AF196976.4 GI:20149791			
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 Db 2061 CAGACCATACCAAGACCAAGATGACGAAATCAATA 2099

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 ACCESSION AC116940.2 GI:27884871  
 VERSION HTG; HTGS PHASE2; HTGS DRAFT.  
 KEYWORDS Pan troglodytes (chimpanzee)

## ORGANISM

## REFERENCE

Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
1 (bases 1 to 194043)

## AUTHORS

Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.,  
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,  
Carraga, K., Coleman, B., Engle, J., Granite, S., Guan, X., Gupta, J.,  
Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E.,  
Laric, P., Lee-Lin, S.-O., Legaspi, R., Maduro, O.L., Maduro, V.B.,  
Margulies, E.H., Mastello, C., Maskeri, B., McDowell, J.,  
Paguirian, C., Pearson, R., Portnoy, M.E., Prasad, A.,  
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Stankirlop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L.,  
Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D.  
NISC Comparative Sequencing Initiative  
Unpublished  
2 (bases 1 to 194043)  
Green, E.D.

## TITLE

Direct Submission

## REFERENCE

Submitted (03-APR-2002) NIH Intramural Sequencing Center, 8717  
GroveMont Circle, Gaithersburg, MD 20877, USA  
3 (bases 1 to 194043)

## AUTHORS

Green, E.D.  
Direct Submission  
Submitted (24-JAN-2003) NIH Intramural Sequencing Center, 8717  
GroveMont Circle, Gaithersburg, MD 20877, USA  
On Jan 24, 2003 this sequence version replaced gi:19909414.

## COMMENT

----- Genome Center  
Center: NIH Intramural Sequencing Center  
Center code: NISC  
Web site: <http://www.nisc.nih.gov>  
Contact: nisc.zoo@nih.gov

----- Project Information  
Project name: c1g

Center project name: c1g

The sequence data in this record represents an 'enhanced'  
version of a Phase 2 submission. Specifically, the indicated  
order and orientation of each sequence contig has been  
established using one or more of the following: read-pair  
data from individual subclones, overlaps with neighboring  
clones, alignment with available reference sequence (e.g.,  
human), and/or confirmation by PCR testing. In addition,  
the sequence assembly is based on at least 8x average  
coverage in Q20 bases and has been reviewed to rule out  
gross misassemblies, the low-quality ends of sequence  
contigs have been trimmed away, and each base is associated  
with a Phrap-derived quality score.

## ----- Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 194018 bases at least Q40  
Consensus quality: 194031 bases at least Q30  
Consensus quality: 194034 bases at least Q20  
Insert size: 173000; agarose-fp  
Insert size: 194043; sum-of-contigs  
Quality coverage: 11.12x in Q20 bases; agarose-fp  
Quality coverage: 9.91x in Q20 bases; sum-of-contigs

-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 1 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
\* 1 194043: contig of 194043 bp in length.

## FEATURES

## source

1. 194043  
Location/Qualifiers  
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vector side:right"  
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AC116436 clone RP43-55P4 (center project name c1f)"  
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BASE COUNT 50907 a 42383 c 41954 g 58799 t  
ORIGIN

## Alignment Scores:

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Score:	3407.00	Matches:	648
Percent Similarity:	99.39%	Conservative:	1
Best Local Similarity:	99.23%	Mismatches:	4
Query Match:	98.87%	Indels:	0
DB:	2	Gaps:	0

US-09-991-053-10 (1-653) x AC116940 (1-194043)

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Db	159980	ATTAACCTCTGTGGAGGTAAGTGTGACCAACCACTGGAAATCCATCTGCTCCG 159921
Qy	21	pheValTyrLeuThrAlaGlnValTrpIleLeuCysAlaAlaIleAlaAlaIleSer 40
Db	159920	TTGCTTACTCTCAGCGGCAAGTGTGATTTCTGTGACGACCTGCTGCGGCTCA 159861
Qy	41	AlaGlyProGlnAsnGlyProSerValCysSerCysSerAsnGlnPheSerValVal 60
Db	159860	GCCGGGCCCCAGAACGCCCCCTCGTGTGTGTGAGTAACCAAGTTCAGCAAGGTG 159801
Qy	61	CysThrArgArgGlyLeuSerGluValProGlnGlyIleProSerAsnThrArgTyrLeu 80
Db	159800	TGCAACCGCGGGGCTTCCAGAGTCCCGGAGGATATTCCTCGAACAACCGGTAC 159741
Qy	81	AsnLeuMetGluAsnAsnIleGlnMetIleGlnAlaAspThrPheArgHisLeuHis 100
Db	159740	AACCTATGGAGAACAAATCCAGATGATCCAGGCGGACCACTCCGCCACCTCCAC 159681
Qy	101	LeuGluValLeuGlnIleuGlyArgAsnSerIleArgGlnIleGluValAlaPheAsn 120
Db	159680	CTGAGAGTCTGTGAGTGGGACAGAACTCATTCGCGAAGTGGGGGCTTCAAC 159621
Qy	121	GlyLeuAlaSerLeuSerThrLeuGluLeuPheAspAsnTrpLeuThrValIleProSer 140
Db	159620	GGCCTGGCCAGCTCAACACCTCGAGCTGTTGCAACATCGGTGACAGTCACTTAC 159561
Qy	141	GlyAlaPheGluTyrLeuSerIleuArgGluLeuTrpLeuArgAsnProIleGlu 160
Db	159560	GGGGCTTTGAATATCACTGTCACAGCTGCGGAGCTCTGGCTTGCAACACCCATCGAA 159501
Qy	161	SerIleProSerTyrAlaPheAsnArgValProSerLeuMetArgLeuAspLeuGlyGlu 180
Db	159500	AGCATCCCTCTTACGCTTCAACCGGGTCCCTCCCTCATGGGCTTGCACTGGGGAG 159441
Qy	181	LeuLysLeuLeuGluTyrIleSerGluGlyAlaPheGluGlyLeuPheAsnLeuLysTyr 200
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Qy	201	LeuAsnLeuGlyMetCysAsnIleLysAspMetProAsnLeuThrProLeuValGlyLeu 220
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QY	221	GIUGIULEUGLIMESERGIYASNHISPEPROGILILERRGPROGISERPHENISGLY	240
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QY	241	LEUSERSERLEULYALYALUTRVALIMETASNSERGINVALISERLEULILEGIUARGSN	260
Db	159260	CTGAGACTCCCTCAGAGAACCTGTGGGTCAATGAATCCACAGGTCAGCCGATTTGAGCGGAAT	159201
QY	261	ALAAPHENAGIYLEUHLASERLEUVALGILEUASNLLEUHLAHISANANLEUSERSER	280
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QY	301	PROTPASNCYASAPCYASAPLILEUUTRPLEUALATPTTRPLEUARGIUTYILEPRO	320
Db	159080	CCTTGAACTGATGTGACATTTCTGTGGCTAGCTGGGTGGCTTGAGAGATATACCC	159021
QY	321	THRAENSERTHCYEGYEGIYARGCYSHISALAPROMETHISHETARGIYARGTYLLEU	340
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QY	361	ASPLEUASNLISERGIUJIYARGMETAGILEULEYSCYARGTHPROPROMETSER	380
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QY	381	SERVALVSTTRPLEUENUPROAHNGIYTHRVALLEUSERHISALASERARGHISPROARG	400
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QY	401	ILESERVALLEUASNSPGIYTHRVLEUASNPHERSHIVALLEUUSERAPBTHRGY	420
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QY	421	VALIYTRTHCYAMETGLYTHRASVALAGIYASNSERASNLASERATATRYLEUASN	440
Db	158720	GTGTACACATGATGTGTGACCAATGTTGACGAGCACTCCAAACGCTGGGCTACCTCAAT	158661
QY	441	GLYSERTHRALGILEUENHTRSERASHTYRSERPHERTHRTRGIYTHRGYGLU	460
Db	158660	GTGACACACGGCTGAGCTCAACCTCCCACTACAGCTTCTTCCACACAGTACAGTGGAG	158601
QY	461	THTRTHGINLISERPROGUASPTTRTHARGIYFTYLYASPROVALPROTHRTHRSER	480
Db	158600	ACCACGGAGATCTCGCTTAGGACACACGCGAAGACAGAGCTGTCTCTACACACGTCC	158541
QY	481	THRGIYTRGILNPROALATYTRTHTRHSERTHTRVALLEULIEGINTHTRARGVAL	500
Db	158540	ACTGTTTACCACCGGSCATATACCACTCTACCAAGTGTCTATCAGACACACCCGTGTG	158481
QY	501	PROLYGINVALALAVALPROALATHRASPTTHTRASPLYSMETGINTHRSERLEUASP	520
Db	158480	CCCAAGCAGGTGGCAGTACCCCGGACAGACACCACTGACAAAGATGCGACACAGCTGGAT	158421
QY	521	GIUVALMETLYETHRTHIRYSILIELLEIGIYCYSPHEVALALAVALTHRLEUENALA	540
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Db	158240	GCAGAGCAACAGCAGCGCTCCGTCGGGTGATCAGGAGGAGGGGCGAGTAGTGGTCCACA	1581861
Oy	601	LeHIsADPHleIleAsnTYrAsnThrTYrLYSPeALAHIGLYAlAhISTPThrgLU	620
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Oy	621	AAnSerLanGLYAnSerSerLeuHisProthrValIThrThIIIsSerGIubProTYrIlelle	640
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Oy	641	GInTHrHISThrLYSAspLYSeValGlnGUThrgInIle	653
Db	158060	CAGACCATTACCAAGACAGGTACAGGAATCTCANATA	158022
<b>RESULT 6</b>			
LOCUS	AC008039/c		
DEFINITION	AC008039	197346 bp	DNA linear PRI 13-JUL-1999
ACCESSION	AC008039	Homo sapiens clone .SCB-391A5 from 7q31,	complete sequence.
VERSION	AC008039.1	GI:5454236	
KEYWORDS	HTG.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 197346)		
JOURNAL	Iadonato,S.P., Yu,J., Wong,G.K.-S., Magnes,C.L., Green,E.D.,		
REMARK	Green,P. and Oleon,M.V.		
COMMENT	Large-scale MCD Mapping and Sequencing of Human Chromosome 7		
	Unpublished		
	2 (bases 1 to 197346)		
	Bubb,K.L., Desmarais,C.L. and Ramsey,S.A.		
	Direct Submission		
	Submitted (13-JUL-1999) Human Genome Center, University of		
	Washington, Box 352145, Seattle, WA 98195, USA		
	University of Washington Human Genome Center		
	Box 352145 Seattle, WA 98195		
	Contact: Kerry Bubb (kbubb@u.washington.edu)		
	Overlapping Sequences:		

5' : UMGC:RG020124  
3' : UMGC:djs166

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**Sequence Quality Assessment:**

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

Double stranded (DS) coverage:	76.0%
DS or two chemistry coverage:	99.4%
Single stranded regions:	5
Sequence Validation:	7.1%

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. Small fragments below a variable cutoff (approximately 400–600 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragment groups are separated by dashed lines.

PGILL		PCORILL		PNBIL	
FP	Seq	FP	Seq	FP	Seq
791.00	781.00	2109.00	2137.00	1098.00	1086.00
6654.00	6602.00	1669.00	1679.00	3491.00	3477.00



2503.00	2500.00	3656.00	3639.00	7486.00	7407.00
4159.00	4119.00	15855.00	15733.00	2508.00	2514.00
3337.00	3317.00	1077.00	1073.00	1242.00	1234.00
4719.00	4712.00	1643.00	1621.00	3631.00	3600.00
2037.00	2096.00	719.00	716.00	2679.00	2625.00
1545.00	1554.00	13752.00	13555.00	2508.00	2460.00
2037.00	2040.00	19216.00	18409.00	22319.00	20834.00
5266.00	5200.00	13752.00	13590.00	497.00	503.00
3937.00	3868.00	3275.00	3264.00	2462.00	2410.00
6391.00	6299.00	12812.00	12693.00	3286.00	3266.00
4003.00	3914.00	3000.00	2928.00	6688.00	6518.00
2037.00	1995.00	3541.00	3512.00	1742.00	1745.00
7013.00	7145.00	1745.00	1758.00	9589.00	9457.00
3476.00	3413.00	9339.00	9200.00	3286.00	3186.00
2037.00	1989.00	19216.00	20057.00	2778.00	2727.00
12384.00	12220.00	13752.00	13370.00	3198.00	3103.00
4557.00	4510.00	7307.00	7161.00	692.00	689.00
996.00	990.00	17764.00	17526.00	955.00	942.00
713.00	706.00	5158.00	5168.00	3198.00	3136.00
10016.00	9889.00	12046.00	11905.00	1288.00	1288.00
2456.00	2394.00	21567.00		4779.00	4710.00
1871.00	1866.00	5389.00		5819.00	5734.00
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1871.00	1846.00			11454.00	11202.00
4377.00	4309.00			15482.00	15240.00
713.00	714.00			5047.00	5011.00
1160.00	1165.00			3491.00	3418.00
536.00	540.00			1288.00	1274.00
2037.00	2013.00			5047.00	4963.00
1342.00	1338.00			4519.00	4544.00
2503.00	2398.00			7486.00	7347.00
3121.00	3075.00			6045.00	5989.00
4719.00	4702.00			4314.00	4295.00
3043.00	2974.00			7771.00	7634.00
2378.00	2290.00			955.00	923.00
7664.00	7609.00			2130.00	2120.00

2833.00 ----- 27446.00 -----  
 2828.00 -----  
 688.00 ----- 679.00 -----  
 10654.00 ----- 10507.00 -----  
 9195.00 ----- 9124.00 -----  
 6034.00 ----- 5970.00 -----  
 2037.00 -----  
 7664.00 -----  
 7283.00 -----

Unmatched fragments are due to vector-containing sequences.  
 We expect 3, 1 and 1-2 such fragments in the BglII, EcoRI, and NheI  
 enzyme domains, respectively. The sum of these fragments can be  
 calculated from the sequence of the BAC clone and, in this clone,  
 should be 16733, 23951, and 24537 for the three enzyme domains.

## FEATURES

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## Alignment Scores:

Pred. No.: 1.89e-268 Length: 197346  
 Score: 3407.00 Matches: 648  
 Percent Similarity: 99.39% Conservative: 1  
 Best Local Similarity: 99.23% Mismatches: 4  
 Query Match: 98.87% Indels: 0  
 DB: 9 Gaps: 0

US-09-991-053-10 (1-653) x AC008039 (1-197346)

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 Db 68919 ATGAAGCTCTTGTGGCAAGTAACTGTGACACCACTGGAAATGCCATCTCTGCTCCG 68860  
 Oy 21 PheValTrrLeuThrAlaGlnValTrrPileuCyAlaAlaIleAlaAlaIleAlaSer 40  
 Db 68859 TTCGCTACCTCAACGCGCCCAAGTGTGATTCGTGTGACGACCATGCTGCGCCCTCA 68800  
 Oy 41 AlaGlyProGlnAsnCyProSerValTrrSerCySerSerAsnGlnPheSerLysValVal 60  
 Db 68799 GCCGGGCCCCAGAACCTGCCCTCCGCTGCTGTCGACATGACAGTTCCAGCAAGGTGTG 68740  
 Oy 61 CysThrArgArgLysLeuSerGlyValProGlnGlyLysProSerAsnThrArgTrrLeu 80  
 Db 68739 TGCACGCCCCGGGCTCTCCGAGGTCCCGACGGGTATTCCTCGAACACCCGGTACCTC 68680  
 Oy 81 AsnLeuMetGlyAsnAsnIleGlnMetIleGlnAlaAspThrPheArgHisLeuHisHis 100  
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 Db 67239 ACAGCCCGCGAGCTGTGATGATATCCAGGTGACGAAAGACATCCAGCAGCAACATCC 67180  
 Oy 581 AlaAlaAlaThrAlaAlaProSerGlyValSerGlyGlnGlyAlaValValLeuProThr 600  
 Db 67179 GCAGACACCAACAGAGCTCGCTCGGTATCAGGTAGGGGAGAGTGGCTGCCACA 67120  
 Oy 601 IleHisAspHisIleAsnTrrAsnThrTrrLysProAlaHisGlyAlaHisTrrPrrGln 620  
 Db 67119 ATTATATACATATTAATTAATTAACACTTAACACCAACAGCATGGGCCCACTGACAGAA 67060  
 Oy 621 AsnSerLeuGlyAsnSerLeuHisProThrValThrThrIleSerGlnProTrrIleIle 640  
 Db 67059 AACAGCTGGGGAACCTCTGCAACCCCAAGTCAACCACTATCTCTGAACCTTAATATAT 67000  
 Oy 641 GlnThrHisThrLysAspLysValGlnGlnThrGlnIle 653  
 Db 66999 CAGACCATATCAAGGACAAAGTACAGAAATCAATAATA 66961

RESULT 7  
 AC119063/c AC119063 202911 bp DNA linear HTG 24-JAN-2003  
 LOCUS Pan troglodytes clone RP43-3406, WORKING DRAFT SEQUENCE, 5 ordered  
 DEFINITION pieces.

ACCESSION AC119063  
 VERSION AC119063.2 GI:27884872  
 KEYWORDS HTG; HTGS PHASE2; HTGS DRAFT.  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.

REFERENCE AUTHORS  
 Abtner, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Bhatia, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Carriaga, K., Coleman, B., Engle, J., Grant, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Latic, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masello, C., Maskeri, B., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Sison, C., Stantripp, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L., Weeteb, K.D., Wiggins, L., Young, A. and Green, E.D.  
 NISC Comparative Sequencing Initiative  
 Unpublished  
 2 (bases 1 to 202911)  
 Green, E.D.

REFERENCE JOURNAL  
 TITLE Direct Submission  
 AUTHORS Submitted (24-APR-2002) NIH Intramural Sequencing Center, 8717  
 JOURNAL Government Circle, Gaithersburg, MD 20877, USA  
 REFERENCE 3 (bases 1 to 202911)  
 Green, E.D.

REFERENCE JOURNAL  
 TITLE Direct Submission  
 AUTHORS Submitted (24-JAN-2003) NIH Intramural Sequencing Center, 8717  
 JOURNAL Government Circle, Gaithersburg, MD 20877, USA  
 REFERENCE On Jan 24, 2003 this sequence version replaced gi:20279434.  
 Genome Center

COMMENT Center: NIH Intramural Sequencing Center  
 Center code: NISC  
 Web site: http://www.nisc.nih.gov  
 Contact: nisc\_zoo@nigri.nih.gov  
 Project Information  
 Center project name: clh  
 Center clone name: 034006

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics -----  
 Sequencing vector: plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 201807 bases at least Q40  
 Consensus quality: 202053 bases at least Q30  
 Consensus quality: 202364 bases at least Q20  
 Insert size: 161000; agarose-fp  
 Insert size: 202511; sum-of-contigs  
 Quality coverage: 12.14x in Q20 bases; agarose-fp  
 Quality coverage: 9.65x in Q20 bases; sum-of-contigs

----- NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

FEATURES  
 source  
 1 142978: contig of 142978 bp in length  
 \* 142979 143078: gap of unknown length  
 \* 143079 177245: contig of 34167 bp in length  
 \* 177246 177345: gap of unknown length  
 \* 177346 183641: contig of 6296 bp in length  
 \* 183642 183741: gap of unknown length  
 \* 183742 202665: contig of 18924 bp in length  
 \* 202666 202765: gap of unknown length  
 \* 202766 202911: contig of 146 bp in length.  
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 /clone="RP43-3406"  
 /clone\_1b="RP43"  
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 160163..202911  
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 183742..202665  
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 202766..202911  
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 clone\_end:T7  
 vector\_side:right"

BASE COUNT 51880 a 48474 c 48875 g 53282 t 400 others  
 ORIGIN

Alignment Scores:  
 Pred. No.: 1.97e-268 Length: 202911  
 Score: 3407.00 Matches: 648  
 Percent Similarity: 99.39% Conservative: 1  
 Best local Similarity: 99.23% Mismatches: 4  
 Query Match: 98.87% Indels: 0  
 DB: 2 Gaps: 0

US-09-991-053-10 (1-653) x AC119063 (1-202911)

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 Db 55668 ATGAAGCTCTTGGCGAGTGAAGTGCACACACCTCGAATGCACTGCTCCG 55609

QY 21 PheValTyrLeuThrAlaGlnValTrrPleLeuCyAlaAlaIleAlaIleAlaSer 40  
 Db 55608 TTGCTACTTACACGCGGCAAGTGTGATTTCTGTGCACCATCGTGTCCGCTCA 55449

QY 41 AlGlyProGlnAlaGlnCysProSerValCysSerCysSerAlaGlnPheSerIleVal 60  
 Db 55548 GCGGCGCCAGAACTGCCCTCCGTCGTCTGTGCAAGTTCAGCAAGTGTG 55489

QY 61 CytThrArgArgIleLeuSerGlnValProGlnGlyIleProSerAlaThrArgTyrLeu 80  
 Db 55488 TGCACGCGCGGAGCTCTTCCGAGGTCCGCAAGGATTCCTCGAACACCCGCTTCC 55429

QY 81 AsnLeuMetGlnLeuAlaGlnIleGlnMetIleGlnAlaSerPheArgHisLeuHis 100  
 Db 55428 AACCTATGAGAAACAACATCCAGATGATCCAGCCGACACTTCCGCCACTCCACAC 55369

QY 101 LeuGlnValIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIle 120  
 Db 55368 CTGAGAGTCTGCAAGTGGGCAAGAACTCATCCGAGATGAGTGGGGCTTCAAC 55309

QY 121 GlyLeuAlaSerLeuSerThrLeuGluLeuPheAspAsnTrpLeuThrValIleProSer 140  
 Db 55308 GGCCTGGCCACAGCTGAGCCTGAGCTGTTCAGCACTGGCTGACAGTCATCCCTAGC 55249  
 QY 141 GlyAlaPheGluTrpLeuSerIleLeuArgGluLeuTrpLeuAlaArgAsnProIleGlu 160  
 Db 55248 GGGGCTTTGAAATACCTGTCCAGAGCTGGAGGCTGTGGCTTCGCAACACCCCTCAGAA 55189  
 QY 161 SerIleProSerTrpAlaPheAsnArgValProSerLeuMetArgLeuAspLeuGlu 180  
 Db 55188 AGCATCCCTCTTACAGCTTCAACCGGGTGCCTCCCTCATAGCGCTGAGCTGGGGAG 55129  
 QY 181 LeuIleValLeuGluTrpIleSerGluAlaPheGluIleLeuPheAsnLeuIleTrp 200  
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 QY 201 LeuAsnLeuGluMetCysAsnIleLeuAspMetProAsnLeuTrpProLeuValGluLeu 220  
 Db 55068 CTGAACCTGGAGTGTGCAACATTAAAGACATGCCAATCTCACCCCTGTGGGGCTG 55009  
 QY 221 GluGluLeuGluMetSerGluValAsnIlePheProGluIleArgProGluSerPheIleGlu 240  
 Db 55008 GAGAGCTGGAGATTCAGGAGAACATTTCCCTGAGATCAAGGCTGGCTCTTCATGAGC 54949  
 QY 241 LeuSerSerLeuValLeuLeuTrpValMetAsnSerGluValSerLeuIleGluArgAsn 260  
 Db 54948 CTGAGCTCCCTCAAGAACCTCTGGGCTCATGAACCTCACAGCTCAGCTGATGAGCGGAT 54889  
 QY 261 AlaPheAspGluLeuAlaSerLeuValGluLeuAsnLeuAlaIleAsnAsnLeuSerSer 280  
 Db 54888 GCTTTGACGGAGCTGGCTTCACTGTGGAACCTGAGCCCAATAAACCTCTCTCT 54829  
 QY 281 LeuProIleAspLeuPheThrProLeuArgTrpLeuValGluLeuIleLeuIleHisAsn 300  
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 QY 301 TrpTrpAsnGluAspCysAspIleLeuTrpLeuAlaTrpTrpLeuArgGluTrpIlePro 320  
 Db 54768 CTTTGAACCTGATGTGACATCTGTGGCTGAGCTGTGGCTTGCAGAGATATATACC 54709  
 QY 321 ThrAsnSerTrpCysGluValArgCysHisAlaProMetHisMetArgGluValTrpLeu 340  
 Db 54708 ACCAATTCACCTGTGTGGCGCTGTGATCATCTCCACATGACATCGAGGCGCTACCTC 54649  
 QY 341 ValGluValAspGluAlaSerPheGluCysSerAlaProPheIleMetAspAlaProArg 360  
 Db 54648 GTGAGAGTGAACAGGCTCTCTCCAGTGCCTGCCCCCTTCATCATGAGACGACCTGCA 54589  
 QY 361 AspleuAsnIleSerGluIleArgMetAlaGluLeuIleCysArgTrpProMetSer 380  
 Db 54588 GACCTCAACATTTCTGAGGTCGAGTGGCAGAACTTAAGTGCAGACTCCCCATATGCC 54529  
 QY 381 SerValIleTrpLeuLeuProAsnGluTrpValLeuSerHisAlaSerArgHisProArg 400  
 Db 54528 TCCGGAAGTGTGTCTCCCAATGGGACATGTCTCACACCGCTCCCGCACCAAGG 54469  
 QY 401 IleSerValLeuAsnAspGluTrpLeuAsnPheSerHisValLeuLeuSerAspThrGlu 420  
 Db 54468 ATCTCTGCTCTCAACGAGCAGCTTGAACCTTTCCCGTGCCTTTCAGACACTGGG 54409  
 QY 421 ValIleTrpCysMetGluTrpAsnValAlaGluLeuSerAsnAlaSerAlaTrpLeuAsn 440  
 Db 54408 GTGTACACATCATGTCAGCAATGTTCAGGCAACCTCAACGCTGGCTACTCAT 54349  
 QY 441 GlySerThrAlaGluLeuAsnThrSerAsnTrpSerPhePheThrThrGluTrpGlu 460  
 Db 54348 GTGGACAGGCTGAGCTCAACACCTCCCACTACAGCTTTCACACCACTAACAAGTGGAG 54289  
 QY 461 ThrThrGluIleSerProGluAspThrThrArgIleValIleValProValProThrSer 480  
 Db 54288 ACCACGAGATCTCCCTGAGGACCAACAGGGAAGTCAAGAGCTGTCTTCAACACGCTCC 54229  
 QY 481 ThrGluTrpGluProAlaTrpThrThrSerThrValLeuIleGluThrThrArgVal 500

Db 54228 ACTGTTACAGCGCGGATATACCACTTACCAAGCTGTGCATTCAGACACCGCTGTG 54169  
 QY 501 ProIleGluValAlaValProAlaThrAspThrThrArgIleValIleValProValProThrSer 520  
 Db 54168 CCNAGGAGGTGGAGTACCCGACACAGACCACTCAAGATGACAGACCGCTGAT 54109  
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 Db 54108 GAATCATGAGAACACCAACATCATTTGGCTTTTGGCAGTGAAGCTGTGAGT 54049  
 QY 541 AlaAlaMetLeuIleValPheTrpValLeuArgIleValArgIleGluIleValSer 560  
 Db 54048 GCCCCATGTTGATGCTTCTTAACTTCGTAAAGGAGCAACGAGCGGAGTACAGTC 53989  
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 QY 581 AlaAlaIleThrAlaIleProSerGluValSerGluGluAlaValAlaValLeuProThr 600  
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 Db 53868 ATTCATGACCATATTAATCACTCAACACCTCAACAAACACATGAGGCCCACTGACAGAA 53809  
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 Db 53748 CAGACCATACCAAGACCAAGTACAGAACTCAATA 53710  
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 AC136196 171218 bp DNA linear HTG 30-OCT-2002  
 AC136196 LOCUS  
 DEFINITION  
 Papio anubis clone R41-180M2, WORKING DRAFT SEQUENCE, 6 unordered pieces.  
 AC136196.1 GI:24421697  
 VERSION  
 HTG; HTGS PHASE1; HTGS DRAFT.  
 KEYWORDS  
 Papio anubis (olive baboon)  
 SOURCE  
 ORGANISM  
 Papio anubis  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecoinae; Papio.  
 1 (bases 1 to 171218)  
 REFERENCES  
 AKhter,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Cariaga,K., Coleman,B., Dietrich,N.L., Engle,J., Granite,S., Guan,X., Gupta,J., Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Idol,J.R., Karlins,E., Lalic,P., Lee-Ihn,S.-O., Legaspi,R., Maduro,Q.L., Maduro,V.B., Margulies,E.H., Masello,C., Maseri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Paguirigan,C., Pearson,R., Portnov,M.E., Prasad,A., Reddy-Dugue,N., Schandler,K., Schueler,M.G., Sison,C., Stankisop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W., Vogt,J.L., Walker,M., Wetherby,K.D., Wiggin,L., Young,A., Zhang,L.-H. and Green,E.D.  
 NISC Migraine Sequencing Initiative  
 2 (bases 1 to 171218)  
 TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 Center: NIH Intramural Sequencing Center  
 Center code: NISC  
 Web site: http://www.nisc.nih.gov  
 Contact: nisc\_zoo@nigrl.nih.gov  
 Project Information

Center project name: cgm  
Center clone name: 180M02  
----- Summary Statistics -----  
Sequencing vector: plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye, 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 169986 bases at least Q40  
Consensus quality: 170160 bases at least Q30  
Consensus quality: 170204 bases at least Q20  
Insert size: 16500; agarose-ef  
Insert size: 170718; sum-of-ctnigs  
Quality coverage: 10.39x in Q20 bases; sum-of-ctnigs  
Quality coverage: 10.04x in Q20 bases; sum-of-ctnigs

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 6 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 4638: contig of 4638 bp in length  
\* 4639 4738: gap of unknown length  
\* 4739 24741: contig of 20003 bp in length  
\* 24742 24841: gap of unknown length  
\* 24842 44289: contig of 19448 bp in length  
\* 44290 44389: gap of unknown length  
\* 44390 80907: contig of 36518 bp in length  
\* 80908 81007: gap of unknown length  
\* 81008 126767: contig of 45760 bp in length  
\* 126768 126867: gap of unknown length  
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BASE COUNT 48428 a 37890 c 37538 g 46861 t 501 others  
ORIGIN

Alignment Scores:  
Pred. No.: 5.76e-268 Length: 171218  
Score: 3400.00 Matches: 647  
Percent Similarity: 99.23% Conservatave: 1  
Best Local Similarity: 99.08% Mismatches: 5  
Query Match: 98.67% Indels: 0  
Gaps: 0

US-09-991-053-10 (1-653) x AC136196 (1-171218)

Qy 1 MettysleuLeuTTPGINValThValHshHshHThTTPaanaIaileuLeuPro 20  
Db 5591 ATGAAGCTCTTGCGAGGTAACTGTGACCAACCACTGCAATGCGATCTGCTCCG 5650

Qy 21 PheValTyleuThraIagInValTTPilleuCyaaIaIaIaIaIaSer 40  
Db 5651 GGTGCTACTTCAACGGCGCAAGTGGATCTGTGACACCACTGCTGCGCTCA 5710

Qy 41 AlagIyProGlnanCyProSerValCySerCySeranGlnPheSerValVal 60  
Db 5711 GCGGGGCCCAAGACCGCCCTGCTGTGTCGTGACCAAGTTCAGCAAGGGGTG 5770

Qy 61 CyeThraArgArgIyleuSerGluValProGlnGlyIleProSeranThraArgTyleu 80  
Db 5771 TGACACCGCGGGGCTCTCCGAGTCCCGCAGAGTATTCCTCCCAACCGGTACTTC 5830

Qy 81 AsnLeuMetCyluaAnsnIleGlnMetIleGlnAlaSPThraArgHshHshHsh 100  
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Qy 101 LeuGluValIleuGlnIleuGlyArgAnSerIleArgIleGluValIleGluAlaPheAn 120  
Db 5891 CTGAGGCTCTGCAAGTGGGCAAGAACTCCATCCGCAATTAGGTGGGGGCTTCAT 5950

Qy 121 GlyLeuAlaSerIleuSerThraIleuGluLeuPheAspAnThraValIleProSer 140  
Db 5951 GGCTGGCCAGCTCAACACCTGAGCTGTGACAACTGCTGACAGTATCTTACG 6010

Qy 141 GlyAlaPheGluTyleuSerIyleuArgGluLeuTyleuArgAnAnProIleGlu 160  
Db 6011 GGGGCTTTGAATACCTGTCAAGCTCGGAGCTGTGTTGGCAACACCCATCGAA 6070

Qy 161 SerIleProSerTyleuAlaPheAnArgValProSerIleuMetArgLeuAspLeuGlu 180  
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Qy 201 LeuAnIleuGlyMetCyaaAnIleuYAspMetProAnIleuThraProleuValGlyLeu 220  
Db 6191 CTGAACCTGGGCACTGTCAACATTAAGACATGCCAATCTCACCCCTGTGGGGCTG 6250

Qy 221 GluGluIleuGluMetSerGlyAnsnHshPheProGluIleuArgProGlySerPheHshGly 240  
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Qy 261 AlaPheAspGlyLeuAlaSerIleuValGluLeuAnIleuAlaHshAnAnIleuSerSer 280  
Db 6371 GCTTTTACGGGCTGGCTTCACTTGTGAACTCAACTTGGCCCAATTAACCTCTTCT 6430

Qy 281 LeuProHshAspLeuPheThraProleuArgTyleuValGluLeuHshHshHsh 300  
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Qy 301 ProTTPAnCyAspCyAspIleuTyleuTyleuAlaTTPTyleuArgIuTyleuPro 320  
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Qy 321 ThraSerThraCyAspGlyArgCyAnHshAlaProMetHshMetArgIyleuTyleu 340  
Db 6551 ACCAATTCACCTGCTGTGGCGCTGTGATGCTCCATGCAATGCAAGCGCGTACTTC 6610

Qy 341 ValGluValAspGlnAlaSerPheGlnCySerAlaProPheIleuMetAspAlaProArg 360  
Db 6611 GTGAGAGTGACCAAGGCTCTTTCAGTGTCTGCTCCCTTCATCATGATGCGCTGCA 6670

Qy 361 AspLeuAnIleuSerGluIyleuMetAlaGluLeuIyleuCyAspArgTTPProPheMetSer 380  
Db 6671 GACCTCAATATTTCTGAGGGTGGATGCAAGACTTAAAGTGTGCACTCCCTATATGTC 6730

Qy 381 SerValIyleuTyleuProAnGlyThraValIleuSerHshAlaSerArgHshProArg 400

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Qy      401 1156rVal1LeuAnaApglyThrLeuAmpHseSerHsVal1LeuLeuSerAepThg1y 420
Db      6791 ATCTCTGTCTCAACGAGGACGACCTTGAATCTTTCACAGCGTGTCTTTCAGACACGTGG 6850
Qy      421 Val1yThrCysWecg1yThrAsnVal1Agl1yAsnSerAsn1Aser1Aly1yLeuAsn 440
Db      6851 GTATACACATGACATGATGACCAATGTGGAGGCAACTCCACGCTGGCTACTTAAT 6910
Qy      441 GlySerThr1Agl1yLeuAsnThr1SerAsn1ySerPhePheThr1yThg1yGlu 460
Db      6911 GTGAGCAGCGCGCGCTCAACACCTCCACATCAGCTTCTTCCACCAAGTAAACAGTGAG 6970
Qy      461 ThrThrGlu1Ser1ProGlu1AepThr1ThrArg1ySer1yAsp1yProVal1ProTh1Ser 480
Db      6971 ACCACGAGATCTGCTCTGAGGACACACGGAAGTACAGGCTGTCTTCTTCCACACGTCC 7030
Qy      481 ThrG1yTyrGlnProAla1yTyrThr1SerThrThrVal1Leu1GlnThrThrArgVal 500
Db      7031 ACTGGTATACAGCGCGCATATACACCTCTACACGAGTCCATTCAGACCAACCGGTG 7090
Qy      501 Pro1yGlnVal1A1Aval1ProAla1Thr1AspThr1Thr1Asp1yWec1GlnThr1Ser1Leu1Asp 520
Db      7091 CCCAGACAGGTGAGTACCGCGCAGACAGACCACTGACAAAGATGACAGACCAAGCTGGAT 7150
Qy      521 Glu1Val1Met1ySerThr1yVal1le1le1Gly1yAsp1yHsVal1Aval1Thr1Leu1A1A 540
Db      7151 GAAGTCATGAGAGACACCAAGATCATATATGAGCTGTGTGGAGAGTACTGTGCTGCT 7210
Qy      541 AlA1A1A1Met1yLeu1Val1Phe1yTyr1yLeu1yArg1yAsn1yGln1yAsn1ySerThr1yVal 560
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Db      7271 ACAGCCCGCGGACTGTGAGATTATCCAGGTGACAGACATCCAGACGACAAATCC 7330
Qy      581 AlA1A1A1Thr1yVal1A1A1Pro1yVal1Ser1yGln1yVal1Aval1Val1Leu1ProThr 600
Db      7331 GCGAGCAGCAACAGACGCTCCGTCGAGTATCAGGTAGAGGAGGAGTATGCTGCCACA 7390
Qy      601 1156rAsp1y1A1A1A1yAsn1yThr1yTyr1yAsn1yPro1A1A1G1yVal1A1A1STpThg1y 620
Db      7391 ATTCTATACCATATTAATTAATCACTACCACTTCAACAGACATGAGGCGCCACTGACAGAA 7450
Qy      621 AsnSer1yGln1yAsnSer1yLeu1yAsp1yProThr1yVal1Thr1y1Ser1yGln1yPro1yTyr1le1le 640
Db      7451 AACAGCCTGGGGAACCTCTGACACCCACAGTCCACACTATCTCTGAACCTTATATATT 7510
Qy      641 GlnThr1yThr1yAsp1yVal1Gln1yThr1Gln1le 653
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RESULT 9
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LOCUS      Papio anubis clone RP41-365M11, WORKING DRAFT SEQUENCE, 3 ordered
DEFINITION
pieces.
AC114887
AC114887.2 GI:27311264
HTG: HTGS PHASE2: HTGS DRAFT.
SOURCE     Papio anubis (olive baboon)
ORGANISM   Papio anubis
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Papio.
1 (bases 1 to 176123)

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REFERENCE
AUTHORS   Akhter,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M.,
          Benjumin,B., Blakeley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
          Cariga,K., Coleman,B., Engle,J., Granter,S., Guan,X., Gupta,J.,
          Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Idol,J.R., Karlins,E.,

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TITLE     JOURNAL
JOURNAL   Submitted (13-MAR-2002) NIH Intramural Sequencing Center, 8717
AUTHORS   Green,E.D.
REFERENCE 2 (bases 1 to 176123)
TITLE     Direct Submission
JOURNAL   Submitted (13-MAR-2002) NIH Intramural Sequencing Center, 8717
AUTHORS   Green,E.D.
REFERENCE 3 (bases 1 to 176123)
TITLE     Direct Submission
JOURNAL   Submitted (21-DEC-2002) NIH Intramural Sequencing Center, 8717
COMMENT   On Dec 20, 2002 this sequence version replaced gi:19387614.
          ----- Genome Center
          Center: NIH Intramural Sequencing Center
          Center code: NISC
          Web site: http://www.nisc.nih.gov
          Contact: nisc.zoo@nih.gov
          Project Information
          Center project name: cgm
          Center clone name: 365M11

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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

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----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 175684 bases at least Q40
Consensus quality: 175833 bases at least Q30
Consensus quality: 175901 bases at least Q20
Insert size: 167000; agarose-fp
Insert coverage: 11.26x in Q20 bases; agarose-fp
Quality coverage: 10.65x in Q20 bases; sum-of-contigs

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* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 39498: contig of 39498 bp in length
* 39499 39598: gap of unknown length
* 39599 158637: contig of 119039 bp in length
* 158638 158737: gap of unknown length
* 158738 176123: contig of 17386 bp in length.

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DB:               2             Gaps:        0

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 REFERENCE 1  
 AUTHORS Wang, J.  
 JOURNAL Thesis (2000) Zhongshan Medical University, Guangzhou, China  
 REFERENCE 2 (bases 1 to 2294)  
 AUTHORS Wang, J.  
 TITLE Direct Submission  
 JOURNAL Submitted (24-OCT-2000) Wang J., Cancer Research Institute, Central  
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 Changsha, Hunan 410078, CHINA  
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* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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* 43222 5187: contig of 11966 bp in length
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* 141690 141789: gap of unknown length
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US-09-991-053-10 (1-653) x AC135841 (1-155852)
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QY 421 ValIYrThrCysMetGlyThrAsnValAlaGlyAsnSerAsnAlaSerAlaTyrLeuAsn 440
Db 106118 GTATATACATGACATGAGCAACAGTGGCAGTAACTCAACGCTGGGCTTACTCAAT 106059
QY 441 GlySerThrAlaGluLeuAsnThrSerAsnIstYrPhePheThrThrGlyThrGlyGlu 460
Db 106058 GTGAGCAGCGCGGCTCAACACTCACTAATATGTTCTTCACTGACATGTCACAGTGAG 105999

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QY 461 ThrThrGluIleSerProGluAspThrThrArgIleTyrIleProValProThrThrSer 480  
 Db 105998 ACCACCGAGATCTCAGCTGAGATACACCGGAAATACAGAGCTGTTCTCAGTACTCT 105939  
 QY 481 ThrGlyTyrGlnProAlaTyrThrThrSerThrThrValIleIleGlnThrThrArgVal 500  
 Db 105938 ACAGGTTATCAGCCGCGCATATACCATCTTACCCAGCTGCTCATTTACAGACCCGCTGTG 105879  
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 Db 105878 CCCAGCAG-----GTACCCGACACGACACCATATATAGATGACAGCCAGCTGGAT 105825  
 QY 521 GluValMetIleThrThrIleIleIleGlyCysAspValAlaValThrIleIleAla 540  
 Db 105824 GAGGTATGAGAACACACAGATCATATGCGCTTTGTGGCAGAGTCTGCTGCT 105765  
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 Db 105764 GCGGCGCATGTGTGATTTCTTCTTAAACTTCGGAAGCGGACCCAGACGAGATACAGTC 105705  
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 Db 105704 ACAGCCCGCCGAGACGTTGAGATTATCAGGTGATGATGACATCCAGCGCGCGTCT 105645  
 QY 581 AlaAlaIleThrAlaIleProSerGlyValSerGlyGluGlyAlaValIleProThr 600  
 Db 105644 GCGACGACACAGAGCTCCATCCGCTGTATCAGTACGAGGCGGACGATGCTGCCACA 105585  
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 Db 105584 ATTCAATGACCATTTAATCACTACACACCTACACACATGAGGCGCCACTGGACAGAA 105525  
 QY 621 AsnSerIleGlyAsnSerIleIleIleProThrValThrIleSerGluProTyrIleIle 640  
 Db 105524 AACAGCTGAGGAACTCTGACCCACAGTTACCAACTCTGAACTTATATATA 105465  
 QY 641 GlnThrIleThrIleAspIleValIleGlnIleIleIleIleIleIle 653  
 Db 105464 CAGACCCATACAGACGACGATACAGAACTCAATA 105426  
 RESULT 12  
 AC137913/c  
 LOCUS  
 DEFINITION Felis catus clone RP86-316B11, WORKING DRAFT SEQUENCE, 10 ordered pieces.  
 AC137913 159915 bp DNA linear HTG 18-MAR-2003  
 VERSION AC137913.2 GI:29029256  
 KEYWORDS HTG; HTGS PHASE2; HTGS\_DRAFT.  
 SOURCE Felis catus (cat)  
 ORGANISM Felis catus  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteleia; Carnivora; Fissipedia; Felidae; Felis.  
 REFERENCE  
 AUTHORS Ahlter, N., Antocletis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakeley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Carisga, K., Coleman, B., Engle, J., Grant, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Katlins, E., Latic, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, C., Pearson, R., Maskeri, B., McDowell, J., Peguigian, C., Pearson, R., Portnoy, M.E., Prasad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Simon, C., Stancic, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D.  
 NISC Comparative Sequencing Initiative  
 TITLE Unpublished  
 JOURNAL  
 REFERENCE  
 AUTHORS Green, E.D.  
 TITLE Direct Submission  
 JOURNAL  
 REFERENCE  
 AUTHORS Submitted (04-DEC-2002) NIH Intramural Sequencing Center, 8717  
 Groveomont Circle, Galtersburg, MD 20877, USA  
 3 (bases 1 to 159915)  
 Green, E.D.

# TITLE JOURNAL COMMENT

Direct Submission  
 Submitted (18-MAR-2003) NIH Intramural Sequencing Center, 8717  
 Groveomont Circle, Galtersburg, MD 20877, USA  
 On Mar 18, 2003 this sequence version replaced gi:26024162.

----- Genome Center  
 Center: NIH Intramural Sequencing Center  
 Center code: NISC  
 Web site: http://www.nisc.nih.gov  
 Contact: nisc.zoo@nih.gov  
 ----- Project Information  
 Center project name: con  
 Center clone name: 316B11

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics  
 Sequencing vector: plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 15812 bases at least Q40  
 Consensus quality: 158745 bases at least Q30  
 Consensus quality: 158971 bases at least Q20  
 Insert size: 142000; agarose-fp  
 Insert size: 159015; sum-of-contigs  
 Quality coverage: 11.74x in Q20 bases; agarose-fp  
 Quality coverage: 10.49x in Q20 bases; sum-of-contigs

-----  
 \* NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and the accession number will be preserved.  
 1 36987: contig of 36987 bp in length  
 \* 36988 37087: gap of unknown length  
 \* 37088 48198: contig of 11111 bp in length  
 \* 48199 48298: gap of unknown length  
 \* 48299 60957: contig of 12659 bp in length  
 \* 60958 61057: gap of unknown length  
 \* 61058 64816: contig of 3759 bp in length  
 \* 64817 64916: gap of unknown length  
 \* 64917 84932: contig of 20016 bp in length  
 \* 84933 85032: gap of unknown length  
 \* 85033 88825: contig of 3793 bp in length  
 \* 88826 88925: gap of unknown length  
 \* 88926 120284: contig of 31358 bp in length  
 \* 120284 120383: gap of unknown length  
 \* 120384 122415: contig of 2032 bp in length  
 \* 122416 122515: gap of unknown length  
 \* 122516 155807: contig of 33222 bp in length  
 \* 155808 155907: gap of unknown length  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9685"  
 /clone="RP86-316B11"  
 /clone\_1b="RP86"  
 1. 37595

misc\_feature

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 /note="assembly\_fragment  
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 /note="assembly\_fragment"  
 misc\_feature 48299. .60957  
 /note="assembly\_fragment"  
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 misc\_feature 85033. .88825  
 /note="assembly\_fragment"  
 misc\_feature 88926. .120283  
 /note="assembly\_fragment"  
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 misc\_feature 122516. .155807  
 /note="assembly\_fragment"  
 misc\_feature 155908. .159915  
 /note="assembly\_fragment"  
 misc\_feature clone end:SP6  
 vector side:right"

BASE COUNT 38366 a 39285 c 39025 g 42339 t 900 others  
 ORIGIN

Alignment Scores:  
 Pred. No.: 2.4e-263 Length: 159915  
 Score: 3343.50 Matches: 639  
 Percent Similarity: 98.32% Conservative: 3  
 Best Local Similarity: 97.86% Mismatches: 8  
 Query Match: 97.03% Indels: 3  
 DB: 2 Gaps: 2

US-09-991-053-10 (1-653) x AC137913 (1-159915)

Qy 1 MetlyseLeuLeuTTPGlnValThrValHshshsthrTPRANAAlleLeuLeuPro 20  
 Db 88454 ATGAAGCTCTTGCGCAGTAACTGTG---CACCCACCTGGAATGCCGCTGCTCC 88398  
 Qy 21 PheValTyrLeuThrAlaGlnValTrrlleuCyseAlaAlaAlaAlaSer 40  
 Db 88397 GTGCTTACCTCAGCGCCAGTGTGATCTGTGTGCAAGCATCGCGCTGCCCTCC 88338  
 Qy 41 AlaGlyProGlnAenCyPProSerValCySerCySerAenGlnPheSerIleVal 60  
 Db 88337 GCCCGGCCCAAGATGCCCATCCCTTGCTCGTGCATTAACCACTTACGCAAGGTGTG 88278  
 Qy 61 CysThrArgArgIleuSerGluValAProGlnGlyIleProSerAenThrArgTyrLeu 80  
 Db 88277 TGCAACCCCTCGGGGCTCTCCGAGGTCCCTCAGGGTATTCCTCCAAACCCGGTACTC 88218  
 Qy 81 AenLeuMetGluAenAenIleGlnMetIleGlnAlaAerThrPheArgHshshsh 100  
 Db 88217 AACCTCAGGAAACAAATATCAATGATCAAGCGGCAACCTTTCGCACTCCACAC 88158  
 Qy 101 LeuGluValLeuGlnLeuGlyArgAenSerIleArgGlnIleGluValAlaPheAen 120  
 Db 88157 CTGAGGCTCTGCACTGGCAGAACTCCATCCGCGCATCGAGTGGGGGCTTCCAC 88098  
 Qy 121 GlyLeuAlaSerLeuSerThrLeuGluLeuPheAenAenThrPLeuThrValIleProSer 140  
 Db 88097 GGCTGGGCGACCTCAACACCTGAGCTGTTCGACTGCTGACAGTATCCCGCAGT 88038  
 Qy 141 GlyAlaPheGluTyrLeuSerIleLeuArgGluLeuTrrPLeuAlaGlnAenProIleGlu 160  
 Db 88037 GGGGCTTTGAGTACTGTCAAGCTGCGGAGCTGTGGCTTCGCAACCAACCATAGAA 87978

Qy 161 SerIleProSerTyrAlaPheAenArgValProSerLeuMetArgLeuAenPLeuGlyGlu 180  
 Db 87977 AGTATCCCTCTTATGCTTCAACCGGGTGCCTCCCTCATGCGCTTGAGCTGGGGAG 87918  
 Qy 181 LeuValysLeuGluTyrIleSerGlnGlyAlaPheGluTyrLeuPheAenLeuTyr 200  
 Db 87917 CTCAGAGGTGAGATCATCTCGAGGGGCTTTTGAAGGAGACTGTTCACCTCAATAC 87858  
 Qy 201 LeuAenLeuGlyMetCyseAenIleLysAenMetProAenLeuThrProLeuValGlyLeu 220  
 Db 87857 CTGAACTGGGCACTGTCACCATTAAGAATATGCCAATCTGACCCCTGCTGGGGCTG 87798  
 Qy 221 GluGluLeuGluMetSerGlyAenHshshPheProGlnIleArgProGlySerPheHshsh 240  
 Db 87797 GAGGAGCTGAGATGTGAGGGAACCACTTCCTGAGATCAAGCGCTGCTCCACAGGC 87738  
 Qy 241 LeuSerSerLeuValysLeuTrrPValMetAenSerGlnIleSerLeuIleGluArgAen 260  
 Db 87737 CTCAGCTCCCTCAGAGCTTTGGGTATGAATCAACAGGTCAAGCTGATAGCGGAC 87678  
 Qy 261 AlaPheAenGlyLeuAlaSerLeuValGluLeuAenLeuAlaHshshAenLeuSerSer 280  
 Db 87677 GCTTTTATGGGCTGGCTCCTCATCTTGGAATCAACTGACCTGGCCCAATACCTCTTCT 87618  
 Qy 281 LeuProHshshPheLeuPheThrProLeuArgTyrLeuValGluLeuHshshshAen 300  
 Db 87617 TTGCCCCATGACCTTCAACCCCACTGAGTACTTGTGAGTTCACCTTACACCAAT 87558  
 Qy 301 ProTrrPancCyseAenPLeuAenIleLeuTrrPLeuAlaTrrPTrPLeuAlaGlyTyrIlePro 320  
 Db 87557 CCCCGAACTGCGATTGTGCAATTCTGGCTGAGCTGCGGTGGCTTGGGAGTACATACC 87498  
 Qy 321 ThrAenSerThrCyseGlyArgCyseHshshAlaProMetHshshMetArgGlyArgTyrLeu 340  
 Db 87497 ACCAATCTTACTGCTGCGCGCGCTGCACTGCTCCCTGCAATGCTGGCCGCTTACTG 87438  
 Qy 341 ValGluValAenGlnAlaSerPheGlnCyseSerAlaProPheIleMetAenAlaProArg 360  
 Db 87437 GTGAGGTGAGCAGAGGCTCTTCCAGTGTCTGCGCTTCATCATGATGAGCCCTCGG 87378  
 Qy 361 AenLeuAenIleSerGluGlyArgMetAlaGluLeuLysCyseArgHshshProPheMetSer 380  
 Db 87377 GATCTCAACATCTCCGAGGTGCGATGCGGAATTAAGTGTGAGTCCCTCCCAATGCTC 87318  
 Qy 381 SerValysTrrPLeuLeuProAenGlyTrrValLeuSerHshshAenSerArgHshshProArg 400  
 Db 87317 TCCGTGAAGTGGCTGCTGCCAATGAGACAGTGTCTGACCAAGCTTCCCGCACCGAGG 87258  
 Qy 401 IleSerValLeuAenAenGlyTrrLeuAenPheSerHshshValLeuLeuSerAenThrGly 420  
 Db 87257 ATCTCTGCTCCCAACGAGCACTTGAATTTTCCACCGTGTCTCAGACACCGGG 87198  
 Qy 421 ValTyrThrCyseMetGlyThrAenValAlaGlyAenSerAenAlaSerAlaTyrLeuAen 440  
 Db 87197 GTATACACTTGCATGAGCAACAGTGGCAGGCACTCCACAGCTGCGCTCACTCAAC 87138  
 Qy 441 GlySerThrAlaGluAenAenThrSerAenTyrSerPhePheThrThrGlyTyrGlyGlu 460  
 Db 87137 GTGAGCAGGCGAGCTCAACCTCCAACTCAAGCTTCTTACCAACAGTCAAGTGGAG 87078  
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 Db 87077 ACCACTAGATCTCACTGAGATACAGACCGGAGATCAAGCTGTTCCTAGAGAGTCC 87018  
 Qy 481 ThrGlyTyrGlnProAlaTyrThrThrSerThrThrValLeuIleGlnThrThrArgVal 500  
 Db 87017 ACTGTTATAGCGCGGATATACACTCCACCAAGCTGTCTCATACAGACACCGCTGTG 86958  
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Db	86903	GAAGTCATGAAGACCAACCAAGATCATTCATGGCTGCTTGTGGCAGATGACTCTGTAAGCT	86844
Qy	541	AlAlAlaMetLeuIleValPheTYrTyrLeuArgIleYargHisGlnGlnArgSerThrVal	560
Db	86843	GCCCCCAATGTTGATGTTCTTCTTCAAACTTCGTAAAGCGGCACAGACAGAGATACAGTC	86784
Qy	561	ThrTrlAlaArgThrValGluIleIleGlnValAlaSerGlnAspIleProAlaAlaThrSer	580
Db	86783	ACACCCCGCCCGACAGTTGAGATCATCAGATGGACCAAAACATCCCAAGCGGGCGGCTCT	86724
Qy	581	AlAlAlaAlaThrAlaAlaProSerGlyValSerGlyGluGlyAlaValValLeuPcoThr	600
Db	86723	GGCGCAGACACAGACAGCTCCGTCGGGTGTATCAGTGTAGGGGGCAGTAGTGTGCCCA	86666
Qy	601	IleHisAspHisIleAsnTYrAsnThrTYrTyrLeuProAlaHisGlyAlaHisStrpThrGlu	620
Db	86663	ATTATATGACCATATTAATTAATCTACAAACACTTACAAACAGCAATGCGGGCCACTGGACAGA	86600
Qy	621	AsnSerLeuGlyIleAsnSerLeuHisProThrValThrThrIleSerGluProTYrIleIle	640
Db	86603	AACGACCTGGGGAACTCTCTGCACCCCGCAGTCCACCATCTGTGAACCTTACATAATT	86544
Qy	641	GlnThrHisThrTyrAspTyrValGlnGlnThrGlnIle	653
Db	86543	CAGACCCATACCAAGACCAAGTACAGAGAACTCAATA	86505
RESULT 13			
AC136203/c			
LOCUS	AC136203	183761 bp	DNA linear HTG 14-NOV-2002
DEFINITION	Bos taurus clone RP42-45B24, WORKING DRAFT SEQUENCE, 5 ordered pieces.		
ACCESSION	AC136203		
VERSION	AC136203.2	GI:24960927	
KEYWORDS	HTG; HTGS_PHASE2; HTGS_DRAFT.		
SOURCE	Bos taurus (cow)		
ORGANISM	Bos taurus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos		
REFERENCE	1 (bases 1 to 183761)		
AUTHORS	Akhter,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Carliaga,K., Coleman,B., Engle,J., Grantte,S., Guan,X., Gupta,J., Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Idol,J.R., Karlins,E., Laic,P., Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L., McDowell,J., Maguiles,E.H., Mastello,C., Maeserl,B., McDowell,V.B., Paduigan,C., Pearson,R., Portnoy,M.E., Prasad,A., Reddix-Digne,N., Schandler,K., Schueler,M.G., Sison,C., Stentridop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W., Vogt,J.L., Wehebydy,K.D., Wiggin,L., Young,A. and Green,E.D.		
TITLE	NISC Comparative Sequencing Initiative		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 183761)		
AUTHORS	Green,E.D.		
TITLE	Direct Submision		
JOURNAL	Submitted (30-OCT-2002) NIH Intramural Sequencing Center, 8717		
REFERENCE	Groveont Circle, Gaitherburg, MD 20877, USA		
AUTHORS	3 (bases 1 to 183761)		
TITLE	Green,E.D.		
JOURNAL	Direct Submision		
REFERENCE	Submitted (14-NOV-2002) NIH Intramural Sequencing Center, 8717		
AUTHORS	Groveont Circle, Gaitherburg, MD 20877, USA		
COMMENT	On Nov 14, 2002 this sequence version replaced gi:24421704.		

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8x average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics

## Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.000310

Assembly program: Philap; version 0.990319  
Consensus quality: 182651 bases at least Q40  
Consensus quality: 182988 bases at least Q30

Insert size: 155000; 220000-  
Consensus quality: 102508 bases at 100%  
Consensus quality: 183248 bases at least Q200

Insert size: 155000; agarose-1p  
Insert size: 183361; sum-of-contigs  
Quality coverage: 10 82x in 020 bases

Quality coverage: 9.15x in Q20 bases; sum-of-contigs

TTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs

represented as runs of  $N$ . The order of the pieces believed to be correct as given, however the sizes

the gaps between them are based on estimates that have been provided by the submittor.

is sequence will be replaced  
the finished sequence as so

1 20735: contig of 20735 bp in length

20736	20835: gap of unknown length
20836	50586: contig of 29751 bp in length

50587	50686: gap of unknown length
50687	80540: contig of 29854 bp in length

80541	80640: gap of unknown length
80641	145873: contig of 65233 bp in length

145874	145973: gap of unknown length
145974	183761: contig of 37788 bp in length

Location/Qualifiers  
1. .183761

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/mol_type="genomic DNA"
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/clone="RP42-45B24"
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clone and .cnc
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[illegible]

6.34e-263      Length: 183761

EV:	98.16%	Conservative:	5
	3339.50	Matches:	636

0  
1  
2  
3  
4  
5  
6  
7  
8  
9

Best Local Similarity: 97.40% Mismatches: 11  
Query Match: 96.91% Indels: 1  
DB: 2 Gaps: 1

US-09-991-053-10 (1-653) x AC136203 (1-183761)

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Db 50137 ATGAAGCTCTTGCGAGGTAACTGTG---CATCAACCTGGAAATGCCGCTCTCCCC 50081  
Qy 21 PheValTYrLeuThrAlaGlnValTroiLeuCyasaalalialaAlaAlaSer 40  
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Qy 41 AlaGlyProGlnAenCyProSerValCySerCySerAenGlnPheSerValVal 60  
Db 50020 GCCGGGCCCAAGATGCCCATCCGTCTGCTGTGTAAACCACTTACGAAGTGTG 49961  
Qy 61 CysThrArgArgIyLeuSerGluValProGlnGlyIleProSerAenThrArgTyrLeu 80  
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Qy 81 AenLeuMetGluAenAenIleGlnMetIleGlnAlaSerThrPheArgHshshsh 100  
Db 49900 AACCTCATGAGAAACAATATCCAGATGATCCAGCGCAACCTTCCGACCTCCACAC 49841  
Qy 101 LeuGluValLeuGlnLeuGlyArgAenSerIleArgGlnIleGluValAlaPheAen 120  
Db 49840 CTGAGAGCTTGTGCACTGGCGAGAACTCCATCCGCGAGATAGAGTGGGGCTTCAAC 49781  
Qy 121 GlyLeuAlaSerLeuSerThrIleuGluLeuPheAenThrPleuThrValIleProSer 140  
Db 49780 GGCCTGGCGAGCTCAACACCTTGAGCTGTGCAACTGGCTGACCGGTATTCACG 49721  
Qy 141 GlyAlaPheGlnTyrLeuSerIyLeuArgIyLeuTyrPleuAArgAenProIleGlu 160  
Db 49720 GGGGCTTGAATACCTGTCCAGAGCTGCGGAGCTGTGCTGCGCAACCCCAATAG 49661  
Qy 161 SerIleProSerTyrAlaPheAenArgValProSerLeuMetArgLeuAspLeuGlu 180  
Db 49660 AGCATCCCTCTTATGCTTCAACCGGGTGCCTCTCATGCGCTGAGCCTGGGGAG 49601  
Qy 181 LeuIyAlyLeuGlnTyrIleSerGlnGlyAlaPheGlnIyLeuPheAenLeuIyTyr 200  
Db 49600 CTCAAGAGCTGAGTACATCTCCAGGGGGCTTTGAGGAGCATTTCAACCTCAAGTAC 49541  
Qy 201 LeuAenLeuGlyMetCysAenIleIyAspMetProAenLeuThrProLeuValGlyLeu 220  
Db 49540 CTGAACCTTGGGATGTGCAACATCAAGAGCATGCCCAACCTCACCTCGTGGGGCTG 49481  
Qy 221 GlnGluLeuGluMetSerGlyAenHshPheProGlnIleArgProGlySerPheHshGly 240  
Db 49480 GAGGAGCTGAGATGTGGGGAAACAATTCCCGGAGATCAAGGCTGCTCTTCAATGGC 49421  
Qy 241 LeuSerSerLeuIyAlyLeuTyrValIleAenSerGlnValSerLeuIleGlnArgAen 260  
Db 49420 CTCGGCTCCCTCAAGAGCTATGGGTCACTGAAGTCAACAAGCTAGCTGATTAAGGGAAT 49361  
Qy 261 AlaPheArgGlyLeuAlaSerIleuValGluLeuAenLeuAlaHshshshshshshsh 280  
Db 49360 GCTTTTGAAGGGCTGGCTCGTGTGTGAATCAACCTGGCCCAATAAATCACTCTCTCT 49301  
Qy 281 LeuProHsh 300  
Db 49300 TTGCCCCATGACCTTTCACCCCTGAGGTACCTGGTGAAGTTGACCTTACCAACCAAT 49241  
Qy 301 ProTyrPasnCyAspCyAspIleLeuTyrPleuAlaTyrTyrPleuArgGlnTyrIlePro 320  
Db 49240 CCTTGAAGCTGATGATGATGATCTCTGCTAGCTGTGCTTCCGGAGATACATACCC 49181  
Qy 321 ThrAenSerThrCyGlyGlyArgGlyArgGlyArgGlyArgGlyArgGlyArgGlyArg 340  
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Qy 341 ValGluValAspGlnAlaSerPheGlnCySerAlaProPheIleMetAapAlaProArg 360  
Db 49120 GTGAGAGGTGACCAAGGCTCTTCCAGTGTCCGCCCCCTTCAATCATGATGCCCTCGG 49061  
Qy 361 AspLeuAenIleSerGlnGlyArgMetAlaGlnLeuIyGlyArgThrProPheMetSer 380  
Db 49060 GACCTCAATATCTCGAGGGGTGGAATGGCGAACTTAAGTGTGAGCTCCCAATGCTC 49001  
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Qy 401 IleSerValLeuAenAspGlyTyrLeuAenPheSerHshshshshshshshshshshsh 420  
Db 48940 ATCTCGCTCTCAACGAGCGACCTTGAATTTTCCACGCTGCTGTGCTGACACAGCG 48881  
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Db 48880 GTATACACGTGCATGTGTGACCAATGTGGCGGCAACTCAATGCTTGGCTTAC 48821  
Qy 441 GlySerThrAlaGluLeuAenThrSerAenTyrSerPheThrThrGlyTyrGlyGlu 460  
Db 48820 GTGAGCAGCGCCGAGCTCAACCTCACTAAGCTTTTTCACACGCTCAAGTGAAG 48761  
Qy 461 ThrThrGluIleSerProGluAspThrThrArgIyTyrIyAspProValProThrThrSer 480  
Db 48760 ACCACGAGATCTGCGCCGAGACACAAACGCGAAGTACAAAGCTGTCTTCAAGACGCTCC 48701  
Qy 481 ThrGlyTyrGlnProAlaTyrThrThrSerThrThrValLeuIleGlnThrThrArgVal 500  
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Qy 501 ProGlnGlnValAlaValProAlaThrAspThrThrAspIyMetGlnThrSerLeuAsp 520  
Db 48640 CCACAGAGGTGGAGTACCGGACCGGACGACCAACGACAAAGATGACAGACAGCTGGAT 48581  
Qy 521 GluValMetIySerThrIyIleIleIleIleIleGlyCysPheValAlaValThrLeuAla 540  
Db 48580 GAATCATGAAGACCAACCAAGATCATCGGCTGCTTGGGAGTACGCTGTGCTGCT 48521  
Qy 541 AlaAlaMetLeuIleValPheTyrIyLeuArgIyArgHshshshshshshshshshshsh 560  
Db 48520 GCTGCATGTGATGTGCTTCTTAATCACTTGCAGAGGGGACCAAGAGAGATACAGT 48461  
Qy 561 ThrAlaAlaArgThrValGluIleIleGlnValAspGluAspIleProAlaAlaThrSer 580  
Db 48460 ACAGCCCGCGGACAGTGTGATATTCAGGTGATATGATCATCTCCGCGCGGACCT 48401  
Qy 581 AlaAlaAlaThrAlaAlaProSerGlyValSerGlyGlnGlyAlaValAlaLeuProThr 600  
Db 48400 GCACACAGACAGCAGCTCCGCGCGGTATCAAGTGAAGGGGAGTGTGCTCCACCA 48341  
Qy 601 IleHsh 620  
Db 48340 ATTCATACCAATATTAATCAACCACTTCAACCAACCAACCACTGAGCGGCAAGAA 48281  
Qy 621 AenSerLeuGlyAenSerLeuHshshshshshshshshshshshshshshshshshshsh 640  
Db 48280 AACAGCTGGGGAATCTTCTTCCACCCCGGCTACCACTATCTTGAACCTTATATCAT 48221  
Qy 641 GlnThrHsh 653  
Db 48220 CAGACCATTCACAGACAGATACAGAAATCAAGTA 48182

RESULT 14  
AC137061 199027 bp DNA linear HTG 21-FEB-2003  
LOCUS Boe taurus clone RP42-517619, WORKING DRAFT SEQUENCE, 5 ordered  
DEFINITION pieces.  
ACCESSION AC137061  
VERSION AC137061.2 GI:28460774  
KEYWORDS HTG; HTGS\_PHASE2; HTGS\_DRAFT.

SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
REFERENCE 1. (bases 1 to 199027)  
AUTHORS Ahter, N., Antonelli, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Carls, K., Coleman, B., Engle, J., Grant, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-I., Ido, J., R., Karling, E., Latic, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q., L., Maduro, V.B., Margulies, E.H., Masello, C., Maskeri, B., McDowell, J., Raguitigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Reddi-Dugue, N., Schandler, K., Schueler, M.G., Sison, C., Stantrop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A., and Green, E.D.  
TITLE NISC Comparative Sequencing Initiative  
JOURNAL Unpublished  
AUTHORS 2. (bases 1 to 199027)  
Green, E.D.  
JOURNAL Direct Submission  
AUTHORS Submitted (15-NOV-2002) NIH Intramural Sequencing Center, 8717  
TITLE Grovemont Circle, Gaithersburg, MD 20877, USA  
JOURNAL 3. (bases 1 to 199027)  
Green, E.D.  
AUTHORS Direct Submission  
JOURNAL Submitted (21-FEB-2003) NIH Intramural Sequencing Center, 8717  
TITLE Grovemont Circle, Gaithersburg, MD 20877, USA  
JOURNAL On Feb 21, 2003 this sequence version replaced g1:25013301.  
COMMENT ----- Genome Center  
Center: NIH Intramural Sequencing Center  
Center code: NISC  
Web site: http://www.nisc.nih.gov  
Contact: nisc\_zoo@nhgri.nih.gov  
Project Information  
Center project name: c1x  
Center clone name: 517G19

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics -----  
Sequencing vector: plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 198351 bases at least Q40  
Consensus quality: 198515 bases at least Q30  
Consensus quality: 198596 bases at least Q20  
Insert size: 183000; agarose-IP  
Insert size: 198627; sum-of-ctnigs  
Quality coverage: 11.14x in Q20 bases; sum-of-ctnigs

----- NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 47170: contig of 47170 bp in length  
\* 47171 47270: gap of unknown length

FEATURES  
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1. 199027  
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/db\_xref="taxon:9913"  
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vector\_side:left  
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/note="clone overlaps with GenBank Accession Number AC136203 clone RP42-45824 (center project name c1y)"  
124556..154564  
/note="assembly\_fragment"  
154665..183154  
/note="assembly\_fragment"  
183255..199027  
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clone\_end:SP6  
vector\_side:right

BASE COUNT 49062 a 46865 c 45878 g 56818 t 400 others  
ORIGIN

Alignment Scores:  
Pred. No.: 7.15e-263 Length: 199027  
Score: 3339.50 Matches: 636  
Percent Similarity: 98.16% Conservative: 5  
Best Local Similarity: 97.40% Mismatches: 11  
Query Match: 96.91% Indels: 1  
DB: 2 Gaps: 1

US-09-991-053-10 (1-653) x AC137061 (1-199027)

Oy 1 MeltyaleuLeuTPrGlnValThrValHisHisThrTrpAsnAlaIleLeuPro 20  
Db 154032 ATGAAGCTCTTGGCAGGTAAGTGTG---CATCACACCTGGAGATGCCGCTGCTCC 153976  
Oy 21 PheValTyrLeuThrValGlnValTrrPileuCYAlaIleAlaIleAlaIleSer 40  
Db 153975 GTGCTTAACTCAGCGGCGCAAGTGTGATTTCTGTGTCAAGCATCGCTGCTGCTCC 153916  
Oy 41 AlaGlyProGlnAsnCyProSerValCySerCySerAsnGlnPheSerIyValVal 60  
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Oy 61 CyThrTrgArgGlyLeuSerGluValPProGlnGlyIleProSerAnThrArgTyrLeu 80  
Db 153855 TGCACCCCGCGGGGCTCTCCAGAGTCTCCAGGGGATTCCTTCCACACCCGCTACTCC 153796  
Oy 81 AsnLeuMetGluAsnAniIleGlnMetIleGlnAlaPheThrPheArgHisIleuHis 100  
Db 153795 AACCTCATGGAGAACATATTCATATTCAGGCGCACCTTCCGCACTTCACACAC 153736  
Oy 101 LeuGluValLeuGlnLeuGlyArgAsnSerIleArgGlnIleGluValGlyAlaPheAsn 120  
Db 153735 CTGAGAGTCTTTCAGAGTGGGAGGAATCTCATCCGAGATAGAGTGGGGGCTTCAAC 153676  
Oy 121 GlyLeuAlaSerLeuSerThrLeuGluLeuPheAspAnThrLeuThrValIleProSer 140  
Db 153675 GGCTTGCGCAGGCTCAACACCTGAGACTGTTCGACCAACTGGCGTGAAGGCTATTCACGC 153616  
Oy 141 GlyAlaPheGluTyrLeuSerIyLeuArgGluLeuThrPheuArgAsnAnProIleGlu 160



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Db 153615 GGGGGCTTGAATACCTGTCAGAGCTGCGGAGCTGCTGCGGACCAACCCATAGAG 153556
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Db 153555 AGCATCCCTCTTATGCTTCAACCGGGTGCCTCTCTCATATGCGCTGAGCTGGGGAG 153496
Oy 181 LeuIlyLeuGluTyrIleSerGluValAphneGluGlyLeuPheAsnLeuIlyTyr 200
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Oy 201 LeuAsnLeuGlyMetCysAsnIleLysAspMetProAsnLeuThrProLeuValGlyLeu 220
Db 153435 CTGAACCTGGGACATGTGCAACATCAAGACATGCCAACCTCACCCCTGTGGGGCTG 153376
Oy 221 GluGluLeuGluMetSerGlyAsnHisPheProGluIleArgProGlySerPheHisGly 240
Db 153375 GAGAGCTGAGAGATGCGGGAGACCATTCGAGAGATCAAGGCTGTGCTCTCCATGGC 153316
Oy 241 LeuSerSerLeuLysLeuTyrValMetAsnSerGluValSerLeuIleGluArgAsn 260
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Oy 261 AlaPheAspGlyLeuAlaSerLeuValGluLeuAsnLeuAlaHisAsnAsnLeuSerSer 280
Db 153255 GCTTTGATGGGCTGGCTCCTGCTGGTGAACCTCAACCTGGCCCATATTAACCTCTTCT 153196
Oy 281 LeuProHisAspLeuPheThrProLeuArgTyrLeuValGluLeuHisLeuHisAsn 300
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Oy 301 ProTyrAsnCysAspCysAspIleLeuTyrPheAlaTyrTyrPheArgGluTyrIlePro 320
Db 153135 CTTTGAACCTGATGATGATGATCTCTGCGTACGCTGTGTGGCTTGGGAGTATACATACC 153076
Oy 321 ThrAsnSerThrCysCysGlyArgCysHisAlaProMetHisMetArgGlyArgTyrLeu 340
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Oy 361 AspleuAsnIleSerGluGlyArgMetAlaGluLeuLysCysArgThrProProMetSer 380
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Oy 401 IleSerValIleuAsnAspGlyThrLeuAsnPheSerHisValLeuLeuSerAspThrGly 420
Db 152835 ATCTCGCTCTCAAGACGAGGACCTTGAACCTTTCACAGTGTGCTCTCAAGACAGGG 152776
Oy 421 ValTyrThrCysMetGlyThrAsnValAlaGlyAsnSerAsnAlaSerAlaTyrLeuAsn 440
Db 152775 GTATACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 152716
Oy 441 GlySerThrAlaGluLeuAsnThrSerAsnTyrSerPhePheThrThrGlyThrGlyGlu 460
Db 152715 GTGAGCAGCGGCGGAGCTCAACCTCCCACTACAGCTTCTTCAACACGCTGACAGTGGAG 152656
Oy 461 ThrThrGluIleSerProGluAspThrThrArgIlyTyrIlyProValProThrThrSer 480
Db 152655 ACCACCGGATCTGCGCGGAGACCAACAGCGGAGTACCAAGCTGTCTTACAGACGCTCC 152596
Oy 481 ThrGlyTyrGlnProAlaTyrThrThrSerThrThrValLeuIleGlnThrThrArgVal 500
Db 152595 ACTGCTTACAGCGGCTTATACACTCTTACAGCGGTCTCATTCACAGACCCCGGTGG 152536
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Oy 521 GluValMetIlyThrThrIlyIleIleIleGlyCysPheValAlaValThrLeuLeuAla 540
Db 152475 GAGTCAATGAGACCAACCAAGATATATATGCGCTGCTTTGTGGAGTACCTTCTGCT 152416
Oy 541 AlaAlaMetLeuIleValPheTyrLysLeuArgIlyAsnHisGlnGlnArgSerThrVal 560
Db 152415 GCTGCATGCTGATTTGCTTCTTATTAACCTTCGCAAGCGGACCGACGAGAGATACAGTC 152356
Oy 561 ThrAlaAlaArgThrValGluIleIleGlnValAspGluAspIleProAlaAlaThrSer 580
Db 152355 ACAGCCCGCGGAGAGTGAATATATCAGATGATATATACACCTCGCGCGGACCT 152296
Oy 581 AlaAlaAlaThrAlaAlaProSerGlyValSerGlyGluGluValAlaValLeuProThr 600
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Oy 601 IleHisAspHisIleAsnTyrAsnThrTyrLysProAlaHisGlyAlaHisTyrThrGlu 620
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Oy 621 AsnSerLeuGlyAsnSerLeuHisProThrValThrThrIleSerGluProTyrIleIle 640
Db 152175 AACGCTGGGGAATCTCTTCAACCCCGCTCACCACTATCTCTGAACCTTATATCAT 152116
Oy 641 GluThrHisThrLysAspLysValGlnGluThrGlnIle 653
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RESULT 15
AC138045/c 183772 bp DNA linear HTG 30-Apr-2003
LOCUS Susecrofa clone RP44-63p3, WORKING DRAFT SEQUENCE, 4 ordered
DEFINITION pieces.
AC138045 AC138045.2 GI:30231284
VERSION HTG; HTGS PHASE2; HTGS_DRAFT.
KEYWORDS Susecrofa (pig)
SOURCE ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 183772)
Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Carls, K.,
Chen, G., Coleman, B., Coleman, H., Engle, J., Granitz, S., Guan, X.,
Hupce, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-U., Hu, P.,
Hurle, B., Idol, J.R., Karlins, E., Kwong, P., Latic, P., Lee-Lin, S.-Q.,
Legaspi, R., Maduro, Q.D., Maduro, V.B., Margulies, E.H., Masello, C.,
Maskeri, B., McDowell, D., Paguirigan, C., Pearson, R., Portnoy, M.E.,
Prasad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K.,
Stison, C., Stenricop, S., Thomas, J.W., Thomas, P.J., Tsipouri, V.,
Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D.
NIH Comparative Sequencing Initiative
Unpublished
2 (bases 1 to 183772)
Green, E.D.
Direct Submission
Submitted (11-DEC-2002) NIH Intramural Sequencing Center, 8717
Government Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 183772)
Green, E.D.
Direct Submission
Submitted (30-APR-2003) NIH Intramural Sequencing Center, 8717
Government Circle, Gaithersburg, MD 20877, USA
On Apr 30, 2003 this sequence version replaced gi:26449080.
COMMENT
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@ngi.nih.gov
----- Project Information
Center project name: cdx

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Center clone name: 063P03

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

## ----- Summary Statistics -----

Sequencing vector: plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 183056 bases at least Q40  
 Consensus quality: 183274 bases at least Q30  
 Consensus quality: 183427 bases at least Q20  
 Insert size: 153000; agarose-fp  
 Insert size: 183472; sum-of-contigs  
 Quality coverage: 11.31x in Q20 bases; agarose-fp  
 Quality coverage: 9.43x in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.

\* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 40972: contig of 40972 bp in length  
 40973 41072: gap of unknown length  
 41073 116218: contig of 75146 bp in length  
 116219 116318: gap of unknown length  
 116319 129207: contig of 12889 bp in length  
 129208 129307: gap of unknown length  
 129308 183772: contig of 54465 bp in length.

## FEATURES

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## BASE COUNT

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## ORIGIN

## Alignment Scores:

Pred. No.: 8,25e-262 Length: 183772  
 Score: 3326.00 Matches: 636

Percent Similarity: 97.12% Conservative: 5  
 Best Local Similarity: 96.36% Mismatches: 11  
 Query Match: 96.52% Indels: 8  
 DB: 2 Gaps: 2

US-09-991-053-10 (1-653) x AC138045 (1-183772)

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QY 21 PheValTyrLeuThrAlaGlnValTrrPileLeuCyAlaAlaIleAlaIleSer 40  
 Db 73064 GTGCTACCTCCGCGGCGCAAGTGTGATCTGTGCGCACCACTCGCTGCGGCTCC 73005

QY 41 ALG1PProGlnInenCyPProSerValCySerCySerLenGlnPheSerValVal 60  
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QY 61 CyThrArgArgGlyLeuSerGluValProGlnGlyLeuProSerAsnThrArgTyrLeu 80  
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QY 221 GluGluLeuGluMetSerGlyAsnHisPheProGluIleArgProGlySerPheHisGly 240  
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QY 241 LeuSerSerLeuValSerLeuTrrValMetAsnSerIleValSerLeuIleGluArgAsn 260  
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QY 321 ThrAsnSerThrCyAspGlyArgCyHisAlaProMetHisMetArgGlyArgTyrLeu 340

Dh 72164 ACCAATTCACCTGCTGTGGCCGCTGTCAACCTCCCTTGACATGCGAGCGGCTACCTG 72105  
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Qy 401 ILeSerValIleAsnAspGlyThrIleuAnPheSerHisValLeuLeuSerAspThrGly 420  
Dh 71924 ATCTCCGTCTCAACGATGGCACTTGAACCTTTTCCACGTGTCTCTTCAGACACCGGG 71865  
Qy 421 ValIleThrCysMetGlyThrAsnValAlaGlyAsnSerAsnAlaSerAlaTyrIleuAn 440  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 22, 2004, 14:09:54 ; Search time 616 Seconds

(without alignments)  
10258.741 Million cell updates/sec

Title: US-09-991-053-9

Perfect score: 2341

Sequence: 1 cactcccccttctgttaat.....ttaagacaaaagtcacaaa 2341

Scoring table:

IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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- 25: /SIDS1/gcgdata/geneeq/geneeqn-emb1/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2341	100.0	2341	21	Human SLIT protein
2	2316.2	98.9	2360	20	CDNA clone cc359.4
3	2244.2	95.9	2607	21	Human SLIT protein
4	2171.8	92.8	2185	21	Human PRO1111.nuc1
5	2171.8	92.8	2185	21	Membrane-bound pro
6	2171.8	92.8	2185	22	Human cDNA sequenc
7	2171.8	92.8	2185	22	Human PRO1111 (UNQ
8	2171.8	92.8	2185	25	CDNA encoding huma

9	2171.8	92.8	2185	25	ACA04242
10	2171.8	92.8	2185	25	ABX89359
11	2171.8	92.8	2185	25	ABX80270
12	2171.8	92.8	2185	25	ABX80774
13	2171.8	92.8	2185	25	ABX81157
14	2171.8	92.8	2185	25	ABX90247
15	2171.8	92.8	2185	25	ABX77858
16	2171.8	92.8	2185	25	ABX79454
17	2171.8	92.8	2185	25	ABX64093
18	2171.8	92.8	2185	25	ABX17057
19	1976.4	84.4	2324	22	AA528823
20	1952.4	83.4	1962	22	AAAD16345
21	1815.8	77.6	2159	22	AA606571
22	1815.8	77.6	2159	24	ABV83908
23	1467.2	62.7	1805	21	AACT73300
24	1333.2	57.0	1356	21	AAA93631
25	1115.2	47.6	1168	22	ABA06744
26	1115.2	47.6	1168	22	AA528872
27	1115.2	47.6	1168	24	ABV84081
28	628	26.8	2083	24	ABX03572
29	628	26.8	2316	25	ABX70472
30	628	26.8	2397	24	ABX62093
31	628	26.8	2450	24	ABX03571
32	628	26.8	2493	22	AAAD21287
33	628	26.8	2756	24	ABX03577
34	628	26.8	3027	24	ABX62087
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38	605	25.8	2851	20	AAAX08687
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#### ALIGNMENTS

RESULT 1  
AAA93620  
AAA93620 strand: DNA; 2341 BP.

16-JAN-2001 (first entry)

Human SLIT protein-like splice variant SECX 3352358-1 DNA.

SECX protein; human; secreted; membrane-associated; cancer;  
proliferation regulator; differentiation regulator; non-malignant tumour;  
immune disorder; autoimmune disease; transplant rejection; AIDS;  
infection; inflammatory disorder; arthritis; hematopoietic disorder;  
skin disorder; cardiovascular disorder; atherosclerosis; restenosis;  
neurological disease; Alzheimer's disease; trauma; wounding;  
spinal cord injury; skeletal disorder; cytotoxic; immunosuppressive;  
anti-HIV; antiinflammatory; antiallergic; antiatherosclerotic;  
neuroprotective; vulnary; antiallergic; antimicrobial; cardiant;  
dermatological; gene therapy; ds.

Homo sapiens.

Key Location/Qualifiers  
CDS 214..2299

/\*tag= a  
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/transl\_except= (pos:2174..2176, aa:taa)  
/note= "Xaa = unknown. Base 2174-2176 correspond to an  
in-frame stop codon"

PN WO20053742-A2.  
 XX 14-SEP-2000.  
 PD  
 XX 09-MAR-2000; 2000WO-US06280.  
 PF  
 XX 09-MAR-1999; 99US-0123667.  
 PR 08-MAR-2000; 2000US-0123667.  
 XX  
 PA (CUPA-) CUPAGEN CORP.  
 XX  
 PI Shinketsu RA;  
 XX  
 DR WPI: 2000-594318/56.  
 P-PsDB: AAB23033.  
 XX  
 PT Novel human membrane associated or secreted polypeptides and  
 PT polynucleotides useful for diagnosis, prevention and treatment of  
 PT pathological states such as cancer, immune, cardiovascular and  
 PT neurological disorders -  
 XX  
 PS Claim 3; Fig 5; 151pp; English.  
 XX  
 CC Sequences AAA93616-A93631 and AAA93673-A93676 represent nucleic acids  
 CC which encode human SECX proteins (AAB33029-B33048). The SECX proteins  
 CC and the invention are either secreted or membrane-associated proteins  
 CC and act as a regulator of cellular proliferation and differentiation. SECX  
 CC proteins or nucleotides are useful for diagnosing the presence of, or  
 CC predisposition to, a disease associated with altered levels of SECX  
 CC proteins and nucleotides. The SECX proteins are also useful to screen  
 CC compounds that modulate SECX activity or expression. The interaction of  
 CC a SECX protein with other cellular proteins may be useful to modulate  
 CC the activity of a partner protein, cellular proliferation, cellular  
 CC differentiation and cell survival. SECX nucleotides are useful for the  
 CC recombinant expression of SECX protein, and may be used to detect SECX mRNA  
 CC or genetic lesions in the SECX gene. They may also be used to modulate  
 CC SECX expression (e.g., using antisense oligonucleotides). SECX nucleic  
 CC acid sequences are also useful for identifying a cell or tissue type in  
 CC a biological sample, and in forensic biology. SECX primers or probes are  
 CC useful for detecting the presence of SECX nucleotides and for screening  
 CC tissue cultures for contamination. Diseases that may be treated or  
 CC prevented using SECX proteins or nucleotides include cancer (e.g.,  
 CC colorectal carcinoma, prostate cancer), benign tumours, immune disorders  
 CC (including autoimmune diseases, transplant rejection, allergies, AIDS),  
 CC infections, inflammatory disorders, arthritis, haematopoietic disorders,  
 CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,  
 CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g.,  
 CC surgical or traumatic wounds, spinal cord injury), and skeletal  
 CC disorders.  
 CC  
 XX  
 SQ Sequence 2341 BP; 565 A; 708 C; 565 G; 503 T; 0 other;  
 Query Match 100.0%; Score 2341; DB 21; Length 2341;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 301 GATTCTGTGTGAGCGCATGCGTCTGCGGCTCAGCGGGGCGCCAGAACTGCGCCCTCCGT 360  
 QY 361 CTGCTGTGTGAGTAACAGTTTCAGCAAGTGTGTGACAGCGCGCGGGCTCTCCGAGGT 420  
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 DB 541 CTCATCCGCGCAGATTGAGTGGGGGCTTCAACGGCTGGCCAGCTCAGCACTCTGA 600  
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 DB 601 GCTGTTGCAACAATGCTGACAGTATCTTAGCGGGGCTTTGAAATCTGTCCAAGCT 660  
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Db 2341 A 2341

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RESULT 2  
AA90848

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KW secreted protein; H23117; human cDNA clone 51970_3; gene therapy;
KW cytokine; nutritional activity; cell proliferation; immune stimulation;
KW immune suppression; hematopoiesis regulation; tissue growth;
KW tumour inhibition; ds.
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PD 07-OCT-1999.
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PF 30-MAR-1999; 99WO-US06946.
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PR 31-MAR-1998; 98US-0080110.
PR 29-MAR-1999; 99US-0280591.
XX
XX (GENY ) GENETICS INST INC.
PI Jacobs K, McCoy JM, LaValle ER, Collins-Racie LA, Evans C;
PI Mesberg D, Treacy M, Agostoino MJ, Steininger RJ;
DR P-PSDB; AAY28806.
XX
XX WPI; 1999-610849/52.
XX
PT Polynucleotides encoding secreted human proteins, derived from human
PT adult brain, human fetal brain, human fetal kidney, and human adult
PT blood cDNA libraries.
XX
XX Claim 1; Page 96-97; 122pp; English.
XX
XX The present nucleotide sequence comprises the full-length protein-coding
XX sequence of clone cc359_4. cc359_4 was isolated from a human adult brain
XX cDNA library using methods specific for secreted protein cDNAs. This
XX demonstrates some similarity with AAX23117 of human cDNA clone 51970_3.
XX This can be used in gene therapy. The polynucleotide and protein may
XX effect nutritional activity, cytokine and cell proliferation, immune
XX stimulation or suppression, hematopoiesis regulation, tissue growth,
XX tumour inhibition etc.
XX
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Best Local Similarity 99.6%; Pred. No. 0;
Matches 2332; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
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1021 GGAACCTCAACCTTGGCCCAAAATTAACCTCTTCTTTGGCCCAATGACTTTTACCCGCT 1080  
1022 GGAACCTCAACCTTGGCCCAAAATTAACCTCTTCTTTGGCCCAATGACTTTTACCCGCT 1081  
1081 GAGGTAACTGTGTGAGTGTGATCTTACACCAACCTTGGAACTGTGATTTGACATTTCT 1140  
1082 GAGGTAACTGTGTGAGTGTGATCTTACACCAACCTTGGAACTGTGATTTGACATTTCT 1141  
1141 GTGGCTAGGCTGTGGCTCTGAGAGTATTAACCAACCAATTCACCTGTGTGGCGGCTG 1200  
1142 GTGGCTAGGCTGTGGCTCTGAGAGTATTAACCAACCAATTCACCTGTGTGGCGGCTG 1201  
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1202 TCATGCTCCCATGACATGCGAGGCGCTAAGCTGTGAGGTGACAGAGCTCTCTTCCA 1261  
1261 GTGCTCTGCGCCCTTATCATATGAGAGCAGCTCGAGACCTCAACATTTTGTGAGGTCGAT 1320  
1262 GTGCTCTGCGCCCTTATCATATGAGAGCAGCTCGAGACCTCAACATTTTGTGAGGTCGAT 1321  
1321 GGCAGAACTTAAGTGTGGGACTCCCTATGTCTCTCGGTGAAGTGTGCTGCCAATGG 1380  
1322 GGCAGAACTTAAGTGTGGGACTCCCTATGTCTCTCGGTGAAGTGTGCTGCCAATGG 1381  
1381 GACAGTGTCAAGCAGCGCTCCCGCACCAGAAATCTGTGTCTTCAACAGAGGACCTT 1440  
1382 GACAGTGTCAAGCAGCGCTCCCGCACCAGAAATCTGTGTCTTCAACAGAGGACCTT 1441  
1441 GAACTTTTCCACGAGTGTGCTTTGAGACACTGGGGGTGACACATGACATGAGGAACTAAT 1500  
1442 GAACTTTTCCACGAGTGTGCTTTGAGACACTGGGGGTGACACATGACATGAGGAACTAAT 1501  
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1562 CAATCAAGCTTTCTTACCAAGAGAAAGGGGAGACCAAGAGATCTTGCTGAGAGAC 1621  
1621 AACGGAAAGTACAAAGCTGTTCCTACCAAGCTTCACTGATTAACGAGCGGATATACAC 1680  
1622 AACGGAAAGTACAAAGCTGTTCCTACCAAGCTTCACTGATTAACGAGCGGATATACAC 1681  
1681 CTCTACCAAGGCTCATTTAGACTACCCGCTGTGCGCAAGAGGTGGAGTACCCGAGC 1740  
1682 CTCTACCAAGGCTCATTTAGACTACCCGCTGTGCGCAAGAGGTGGAGTACCCGAGC 1741  
1741 AGACACCACTGACAAAGATGACAGACCAAGCTGTGATGAATCATGAAGACCAACATCAT 1800  
1742 AGACACCACTGACAAAGATGACAGACCAAGCTGTGATGAATCATGAAGACCAACATCAT 1801  
1801 CATGCGCTGTTTGTGGAGTGAACCTGTGAGCTGCGGCAATGTTGATTTCTTATTA 1860  
1802 CATGCGCTGTTTGTGGAGTGAACCTGTGAGCTGCGGCAATGTTGATTTCTTATTA 1861  
1861 ACTTGTAAGGGGCGACAGAGCGGAGTACGTCAAGCGGCGCGGACTGTGTGAGATTAAT 1920  
1862 ACTTGTAAGGGGCGACAGAGCGGAGTACGTCAAGCGGCGCGGACTGTGTGAGATTAAT 1921  
1921 CCAAGTGAACGAAGACATCCAGACAGCAACATCCGACAGACACAGAGCTCCGTCGG 1980  
1922 CCAAGTGAACGAAGACATCCAGACAGCAACATCCGACAGACACAGAGCTCCGTCGG 1981  
1981 TGTATCAGGTGAAGGGGAGAGTATGAGCTGCGGCAATTCATGACATATTAACAACAC 2040  
1982 TGTATCAGGTGAAGGGGAGAGTATGAGCTGCGGCAATTCATGACATATTAACAACAC 2041  
2041 CTACAAACCAAGACATGAGGCGGCACTGACAGAAACAGCGTGGGAACTCTGACACC 2100  
2042 CTACAAACCAAGACATGAGGCGGCACTGACAGAAACAGCGTGGGAACTCTGACACC 2101  
2101 CACAGTCAACCATATCTTGAACCTTATATTAATTCAGACCAATTCAGAGGACAGAGTACA 2160  
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2161 GGAACCTCAAAATTAAGCTCCCTCCGCAAAAATTTAATAATGCAATGAAATGACAC 2220  
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2282 AAGTCTATGGCTGTGTTAAAAAAAACAGATTAATTAATAATTAAGCAAAAGCTCAA 2340





Db 901 CTTCCCTGAGATCAGGCGCTGCTCCCTCCATGCGCTCCCAAGAACCTCTGCGAT 960  
 Qy 961 CATGAACCTACAGGCTCAGCTGATGAGGGGAAATGCTTTTGAAGGGCTGGCTCACTTGT 1020  
 Db 961 CATGAACCTACAGGCTCAGCTGATGAGGGGAAATGCTTTTGAAGGGCTGGCTCACTTGT 1020  
 Qy 1021 GGAACCTCAACTGGGCCAACAATACCTCTCTTCTTGGCCCAATGACCTCTTTTACCCTGCT 1080  
 Db 1021 GGAACCTCAACTGGGCCAACAATACCTCTCTTCTTGGCCCAATGACCTCTTTTACCCTGCT 1080  
 Qy 1081 GAGGTAACCTGGTGGAGTTGATCTACACCAACCTTGGAACTGTGATTTGACATTTCT 1140  
 Db 1081 GAGGTAACCTGGTGGAGTTGATCTACACCAACCTTGGAACTGTGATTTGACATTTCT 1140  
 Qy 1141 GTGGCTAGCGCTGGCTGGCTGGAGATATATACCAATTCACCTGCTGGCGCGCTG 1200  
 Db 1141 GTGGCTAGCGCTGGCTGGCTGGAGATATATACCAATTCACCTGCTGGCGCGCTG 1200  
 Qy 1201 TCATGCTCCCATGACATGCGAGGCGCTACCTCGTGGAGTGGACAGGCTCTCTTCCA 1260  
 Db 1201 TCATGCTCCCATGACATGCGAGGCGCTACCTCGTGGAGTGGACAGGCTCTCTTCCA 1260  
 Qy 1261 GTGCTCTGCCCCCTTCATCATGAGCGACCTCGAGACTCAACATTTCTGAGGGTGGAT 1320  
 Db 1261 GTGCTCTGCCCCCTTCATCATGAGCGACCTCGAGACTCAACATTTCTGAGGGTGGAT 1320  
 Qy 1321 GGCAGAACCTTAAGTGTGGAATCTCCCTTATGTCCTCGAAGTGTGTCTCCCAATG 1380  
 Db 1321 GGCAGAACCTTAAGTGTGGAATCTCCCTTATGTCCTCGAAGTGTGTCTCCCAATG 1380  
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 Db 1381 GACAGTGTCAAGCAGCGCTCCCGACCAAGATCTGTGCTTCAAGACGACCTT 1440  
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 Db 1441 GAACTTTTCCACAGTGTCTGTTTCAAGACCTGGGGTGTACACATGATGGGACCAATGT 1500  
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 Db 1501 TCGAGCAACTCCAAAGCGCTCGGCTCACTCAATGGGACACGCGCTTAAACCTTC 1560  
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 Qy 1681 CTCTACCAAGGCTCTATTCAGACTACCGGTGTGCCAAGAGAGTGGCAGTACCCCGAC 1740  
 Db 1681 CTCTACCAAGGCTCTATTCAGACTACCGGTGTGCCAAGAGAGTGGCAGTACCCCGAC 1740  
 Qy 1741 AGACACCACTGACAGAGTGCAGACAGCGCTGATGAAGTATGAAGACCAACAGATCAT 1800  
 Db 1741 AGACACCACTGACAGAGTGCAGACAGCGCTGATGAAGTATGAAGACCAACAGATCAT 1800  
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 Db 1801 CATTTGCTGTTTGTGGCAGTGACTGTGAGTGTGCGCGCATTTGATTTCTTATTA 1860  
 Qy 1861 ACTTGTGAAGCGGACCAAGAGCGAGTATGACAGCGG--CCGGAAGTGTGAGTA 1918  
 Db 1861 ACTTGTGAAGCGGACCAAGAGCGAGTATGACAGCGG--CCGGAAGTGTGAGTA 1918  
 Qy 1919 ATCCAGGTGAGAGAGATCCAGAGCAACATCCGAGCAGACACAGAGCTCGCTCC 1978  
 Db 1919 ATCCAGGTGAGAGAGATCCAGAGCAACATCCGAGCAGACACAGAGCTCGCTCC 1978  
 Qy 1921 ACACAGGAGACAAACACACACAAACAAACAAACAAACAAACAAACAGCCCCCCC 1980  
 Db 1921 ACACAGGAGACAAACACACACAAACAAACAAACAAACAAACAAACAGCCCCCCC 1980  
 Qy 1979 GGTGTATCAGGTAGAGGGGAGTGTGCTGCCCAATTCATGACCATTTAATTAACAAC 2038  
 Db 1979 GGTGTATCAGGTAGAGGGGAGTGTGCTGCCCAATTCATGACCATTTAATTAACAAC 2038

Db 1981 GGTATTAACAGGAAGGCAATAGCCGCCCAACAAACACACAAACATTAACAAAC 2040  
 Qy 2039 ACTTACAAACAGACATAGGGGCCCACTGACAGAAAAAGCTGGGGAACTCTGAC 2098  
 Db 2041 ACACAGAAACAGACATAGGGGCCCACTGACAGAAAAAGCTGGGGAACTCTGAC 2100  
 Qy 2099 CCCAGTACACACTATCTGAACTTATTAATTCAGACCCATACAGAGACAGGTA 2158  
 Db 2101 CCCAGTACACACTATCTGAACTTATTAATTCAGACCCATACAGAGACAGGTA 2160  
 Qy 2159 CAGAAATCAAAATATGATCTCCCTCCCAAAAACTTAATAATGATGAAATGAC 2218  
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 Qy 2219 ACAAGACAGCAACTTTTGTACAGAGTGGGAGAGACTTTTCTGTATATGTTATTA 2278  
 Db 2221 ACAAGACAGCAACTTTTGTACAGAGTGGGAGAGACTTTTCTGTATATGTTATTA 2280  
 Qy 2279 TTAAGTCTATGGGCTGTTAAAAAACAGATTAATTAATTAATTAAGACAAAGTCA 2338  
 Db 2281 TTAAGTCTATGGGCTGTTAAAAAACAGATTAATTAATTAATTAAGACAAAGTCA 2340  
 Qy 2339 AAA 2341  
 Db 2341 AAA 2343  
 RESULT 4  
 AAC58383  
 ID AAC58383 standard; cDNA, 2185 BP.  
 XX AAC58383;  
 XX  
 DT 29-JAN-2001 (first entry)  
 XX  
 XX Human PRO1111 nucleotide sequence SEQ ID NO:45.  
 DE  
 XX  
 XX Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;  
 KW proliferation; tumorigenesis; identification; cancer; cytostatic;  
 KW neotropic; neuroprotective; antiinflammatory; immunosuppressive;  
 KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;  
 KW neuronal disorder; glial disorder; astrocytal disorder; angiogenic;  
 KW hypochalamic disorder; glandular disorder; macrophagal disorder;  
 KW epithelial disorder; stromal disorder; blascoellic disorder;  
 KW inflammatory disorder; immunologic disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 PN WO20053755-A2.  
 XX  
 PD 14-SEP-2000.  
 XX  
 XX 06-JAN-2000; 2000MO-US00376.  
 PF  
 XX 08-MAR-1999; 99WO-US05028.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 07-JUL-1999; 99US-0143048.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 05-JAN-2000; 2000MO-US00219.  
 XX  
 PA (GENTH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;  
 PI Watanabe CK, Wood WJ;  
 XX  
 DR WPI, 2000-572270/53.  
 DR F-PSDB; AAB24073.  
 XX  
 PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the  
 treatment, diagnosis and prevention of cancer -



XX Claim 50; Fig 33; 286bp; English.

CC The present invention describes an isolated antibody that binds to  
 CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO355,  
 CC PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,  
 CC PRO1023, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,  
 CC PRO1187, PRO1281, PRO23, PRO39, PRO399, PRO317, PRO1710, PRO2094,  
 CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell  
 CC growth. The PRO polypeptides and nucleotides are useful in the  
 CC treatment, diagnosis and prevention of cancer. The antibodies and other  
 CC anti-tumour compounds may be used to treat various conditions, including  
 CC those characterised by overexpression and/or activation of the amplified  
 CC PRO genes. Exemplary conditions or disorders to be treated with such  
 CC antibodies and other compounds include benign or malignant tumours  
 CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,  
 CC colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic  
 CC carcinomas, sarcomas, glioblastomas, and various head and neck tumours),  
 CC leukaemias and lymphoid malignancies, other disorders such as neuronal,  
 CC glioma, astrocytoma, hypothalamic and other glandular, macrophagal,  
 CC epithelial, stromal and blastocoele disorders, and inflammatory,  
 CC angiogenic and immunologic disorders. AAC58242 to AAC5836 represent PCR  
 CC primers and hybridisation probes used in the isolation of the human PRO  
 CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human  
 CC PRO polynucleotide and protein sequences given in the exemplification of  
 CC the present invention.

XX Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;

Query Match 92.8%; Score 2171.8; DB 21; Length 2185;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 2176; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 159 GTTCTCCCTTCCGAGCAAAATCCAGGCGATGGAATTATGAACTGCGCACACATGA 218  
 DB 1 GTTCTCCCTTCCGAGCAAAATCCAGGCGATGGAATTATGAACTGCGCACACATGA 60  
 QY 219 AGCTCTTGGCAGGTAAGTGTGACACACACCTGGAATGCCATCCGCTCCGCTTG 278  
 DB 61 AGCTCTTGGCAGGTAAGTGTGACACACACCTGGAATGCCATCCGCTCCGCTTG 120  
 QY 279 TCTACTCAGCGCGCAAGTGTGATTTCTGTGACGACCATCGCTCCGCTTGAGCG 338  
 DB 121 TCTACTCAGCGCGCAAGTGTGATTTCTGTGACGACCATCGCTCCGCTTGAGCG 180  
 QY 339 GGGCCCAAACTGCCCCCTCCGCTCTGTGTGATTAACCAAGTTGCAAGGTGTGCA 398  
 DB 181 GGGCCCAAACTGCCCCCTCCGCTCTGTGTGATTAACCAAGTTGCAAGGTGTGCA 240  
 QY 399 CGCGCGGAGGCTCTCCGAGGTCGCGAGGATTTCCCTCGAACACCGGGTACCTCAAC 458  
 DB 241 CGCGCGGAGGCTCTCCGAGGTCGCGAGGATTTCCCTCGAACACCGGGTACCTCAAC 300  
 QY 459 TCATGAGAAACAATCCAGATGATCAAGGCGACACCTCCGCCACTCCACACTTG 518  
 DB 301 TCATGAGAAACAATCCAGATGATCAAGGCGACACCTCCGCCACTCCACACTTG 360  
 QY 519 AGGTCTTCAAGTTGGGCGAAGCTTCATTCGCGAGATTGAGTGGGGGCTTCAACGCGC 578  
 DB 361 AGGTCTTCAAGTTGGGCGAAGCTTCATTCGCGAGATTGAGTGGGGGCTTCAACGCGC 420  
 QY 579 TGGCAGGCTGAGCAGCTCGAGGCTGTGACAACTGAGCTGACATCACTCCCTACGCGGG 638  
 DB 421 TGGCAGGCTGAGCAGCTCGAGGCTGTGACAACTGAGCTGACATCACTCCCTACGCGGG 480  
 QY 639 CTTTGAATACCTGTCAAGCTGCGGAGCTTGTGCTTGCACCAACCCCATCGAAACA 698  
 DB 481 CTTTGAATACCTGTCAAGCTGCGGAGCTTGTGCTTGCACCAACCCCATCGAAACA 540  
 QY 699 TCCCTCTTAAGCCTTCAACCGGGTGGCTCTCATGCGCTTGGAATTGGGGAGCTCA 758  
 DB 541 TCCCTCTTAAGCCTTCAACCGGGTGGCTCTCATGCGCTTGGAATTGGGGAGCTCA 600

QY 759 AGAAGCTGAGTATATCTGTGAGGAGGCTTTTGAGGGGCTGTCAACTCAAGTATCTGA 818  
 DB 601 AGAAGCTGAGTATATCTGTGAGGAGGCTTTTGAGGGGCTGTCAACTCAAGTATCTGA 660  
 QY 819 ACTTGGGATGTGCAACATTAAAGACATGCCAATCTCACCCCTGTGTGGGTGAGG 878  
 DB 661 ACTTGGGATGTGCAACATTAAAGACATGCCAATCTCACCCCTGTGTGGGTGAGG 720  
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 DB 721 AGCTGGAGATTCAGGGGACACACTTCCCTGAGATCAGAGCTGCTCTTCATAGGCGCTGA 780  
 QY 939 GCTCCCTCAAGAACTCTGAGGTCAAGTACAGAGTCAAGCTTATGAGGGAATGCTT 998  
 DB 781 GCTCCCTCAAGAACTCTGAGGTCAAGTACAGAGTCAAGCTTATGAGGGAATGCTT 840  
 QY 999 TTGACGGGCTGGCTTCACTTGTGGAACCTGAACCTTGGCCCAATPACTCTTCTTTC 1058  
 DB 841 TTGACGGGCTGGCTTCACTTGTGGAACCTGAACCTTGGCCCAATPACTCTTCTTTC 900  
 QY 1059 CCCATGACCTTTTACCCTGGTGAAGTACCTGAGTGAAGTGAATCAACCAACCTT 1118  
 DB 901 CCCATGACCTTTTACCCTGGTGAAGTACCTGAGTGAAGTGAATCAACCAACCTT 960  
 QY 1119 GGAACGTGATTTGACATTTCTGTGCTAGGCTGAGTGGCTTCAAGAGTATATACCA 1178  
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 QY 1239 AGGTGAGACAGGCTCTCTTCCAGTGTCTGTGCCCCCTTATATGAGACGCTTGAAGC 1298  
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 DB 1321 ACAATGATGAGGAGCCAAATGTGACAGGCACTCAACGCGCTCGGCTCACTCAATGGA 1380  
 QY 1539 GCAAGGCTGAGCTTAACTCACTTCAAGCTTCTTCAACCAAGAGGAGAGCA 1598  
 DB 1381 GCAAGGCTGAGCTTAACTCACTTCAAGCTTCTTCAACCAAGAGAGAGCA 1440  
 QY 1599 CGAGATCTCCCTGAGGACCAACAGGGAAGTACAGGCTGTTCTTCAAGCTCACTG 1658  
 DB 1441 CGAGATCTCCCTGAGGACCAACAGGGAAGTACAGGCTGTTCTTCAAGCTCACTG 1500  
 QY 1659 GTTACAGCGGCGATATACAGCTCTTACAGGAGTCACTTCAAGCTCACTGAGGCGCA 1718  
 DB 1501 GTTACAGCGGCGATATACAGCTCTTACAGGAGTCACTTCAAGCTCACTGAGGCGCA 1560  
 QY 1719 AGCAGTGGCAGTACCGCGCAGACACCACTGACAGAGTCAAGAGTCAAGCTTGAAG 1778  
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Qy 1899 CCGCCCGGACCTGTTAGATTAATCCAGTGGAGAGACATCCACAGCAATCCGGAG 1958
Db 1741 CCGCCCGGACCTGTTAGATTAATCCAGTGGAGAGACATCCACAGCAATCCGGAG 1800
Qy 1959 CAGCAACAGCAGCTCCGTCGGTGTATCAGTGAAGGGCAGTAGTGTGCCACAAATTC 2018
Db 1801 CAGCAACAGCAGCTCCGTCGGTGTATCAGTGAAGGGCAGTAGTGTGCCACAAATTC 1860
Qy 2019 ATGACCAATATTACTTACCAACACCTTACCAACAGCAGCATGGGCCCACTGGACAGAAAACA 2078
Db 1861 ATGACCAATATTACTTACCAACACCTTACCAACAGCAGCATGGGCCCACTGGACAGAAAACA 1920
Qy 2079 GCGTGGGGAACTCTCTGACCCGACAGTCACAGTACATCTCTGACCTTATATTAATTCAGA 2138
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Db 2041 TAAATGCAATAGATGACACAAAGACGAACTTTGTACAGAGTGGGAGAGACTTT 2100
Qy 2259 TTCTTGTAATGCTTATATTAATTAAGTCTTATGAGTGGGCTGTTAAAAAAGATTAATTTAA 2318
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Qy 2319 AATTTAAGACAAAAAGTCAAAA 2341
Db 2161 AATTTAAGACAAAAAGTCAAAA 2183
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RESULT 5  
AAZ65033  
ID AAZ65033 standard; cDNA; 2185 BP.

AC AAZ65033;

DT 05-APR-2000 (first entry)

DE Membrane-bound protein PRO1111 encoding cDNA.

KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIR ligand;  
pharmacological; receptor immunoadhesin; gene mapping; ss.

OS Homo sapiens.

PN WO963088-A2.

XX WO963088-A2.

PD 09-DEC-1999.

PF 02-JUN-1999; 99WO-US12252.

XX 02-JUN-1998; 98US-0087607.

PR 02-JUN-1998; 98US-0087609.

PR 02-JUN-1998; 98US-0087759.

PR 03-JUN-1998; 98US-0087827.

PR 04-JUN-1998; 98US-0088021.

PR 04-JUN-1998; 98US-0088025.

PR 04-JUN-1998; 98US-0088028.

PR 04-JUN-1998; 98US-0088029.

PR 04-JUN-1998; 98US-0088030.

PR 04-JUN-1998; 98US-0088033.

PR 04-JUN-1998; 98US-0088326.

PR 05-JUN-1998; 98US-0088167.

PR 05-JUN-1998; 98US-0088202.

PR 05-JUN-1998; 98US-0088212.

PR 05-JUN-1998; 98US-0088217.

PR 09-JUN-1998; 98US-0088655.

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PR 10-JUN-1998; 98US-0088722.  
PR 10-JUN-1998; 98US-0088730.  
PR 10-JUN-1998; 98US-0088734.  
PR 10-JUN-1998; 98US-0088738.  
PR 10-JUN-1998; 98US-0088740.  
PR 10-JUN-1998; 98US-0088741.  
PR 10-JUN-1998; 98US-0088742.  
PR 10-JUN-1998; 98US-0088810.  
PR 10-JUN-1998; 98US-0088811.  
PR 10-JUN-1998; 98US-0088824.  
PR 10-JUN-1998; 98US-0088825.  
PR 10-JUN-1998; 98US-0088826.  
PR 11-JUN-1998; 98US-0088858.  
PR 11-JUN-1998; 98US-0088861.  
PR 11-JUN-1998; 98US-0088863.  
PR 11-JUN-1998; 98US-0088876.  
PR 12-JUN-1998; 98US-0088909.  
PR 12-JUN-1998; 98US-0088105.  
PR 16-JUN-1998; 98US-0089440.  
PR 16-JUN-1998; 98US-0089512.  
PR 16-JUN-1998; 98US-0089513.  
PR 17-JUN-1998; 98US-0089532.  
PR 17-JUN-1998; 98US-0089538.  
PR 17-JUN-1998; 98US-0089598.  
PR 17-JUN-1998; 98US-0089599.  
PR 17-JUN-1998; 98US-0089600.  
PR 17-JUN-1998; 98US-0089653.  
PR 18-JUN-1998; 98US-0089801.  
PR 18-JUN-1998; 98US-0089907.  
PR 18-JUN-1998; 98US-0089908.  
PR 19-JUN-1998; 98US-0089947.  
PR 19-JUN-1998; 98US-0089948.  
PR 19-JUN-1998; 98US-0089952.  
PR 22-JUN-1998; 98US-0090246.  
PR 22-JUN-1998; 98US-0090252.  
PR 22-JUN-1998; 98US-0090254.  
PR 23-JUN-1998; 98US-0090349.  
PR 23-JUN-1998; 98US-0090355.  
PR 24-JUN-1998; 98US-0090429.  
PR 24-JUN-1998; 98US-0090431.  
PR 24-JUN-1998; 98US-0090435.  
PR 24-JUN-1998; 98US-0090444.  
PR 24-JUN-1998; 98US-0090445.  
PR 24-JUN-1998; 98US-0090461.  
PR 24-JUN-1998; 98US-0090472.  
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PR 24-JUN-1998; 98US-0090540.  
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PR 25-JUN-1998; 98US-0090676.  
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PR 25-JUN-1998; 98US-0090688.  
PR 25-JUN-1998; 98US-0090690.  
PR 25-JUN-1998; 98US-0090691.  
PR 25-JUN-1998; 98US-0090694.  
PR 25-JUN-1998; 98US-0090695.  
PR 25-JUN-1998; 98US-0090696.  
PR 26-JUN-1998; 98US-0090862.  
PR 26-JUN-1998; 98US-0090863.  
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PR 01-JUL-1998; 98US-0091360.  
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PR 02-JUL-1998; 98US-0091486.  
PR 02-JUL-1998; 98US-0091519.  
PR 02-JUL-1998; 98US-0091626.  
PR 02-JUL-1998; 98US-0091628.  
PR 02-JUL-1998; 98US-0091633.  
PR 02-JUL-1998; 98US-0091646.  
PR 02-JUL-1998; 98US-0091673.  
PR 07-JUL-1998; 98US-0091978.  
PR 07-JUL-1998; 98US-0091982.  
PR 09-JUL-1998; 98US-0092182.
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PR 10-JUL-1998; 98US-0092472.  
 PR 20-JUL-1998; 98US-0093339.  
 PR 30-JUL-1998; 98US-0094651.  
 PR 04-AUG-1998; 98US-0095282.  
 PR 04-AUG-1998; 98US-0095285.  
 PR 04-AUG-1998; 98US-0095301.  
 PR 04-AUG-1998; 98US-0095302.  
 PR 04-AUG-1998; 98US-0095318.  
 PR 04-AUG-1998; 98US-0095321.  
 PR 04-AUG-1998; 98US-0095325.  
 PR 10-AUG-1998; 98US-0095916.  
 PR 10-AUG-1998; 98US-0095929.  
 PR 10-AUG-1998; 98US-0096012.  
 PR 11-AUG-1998; 98US-0096143.  
 PR 11-AUG-1998; 98US-0096146.  
 PR 12-AUG-1998; 98US-0096329.  
 PR 17-AUG-1998; 98US-0096757.  
 PR 17-AUG-1998; 98US-0096766.  
 PR 17-AUG-1998; 98US-0096768.  
 PR 17-AUG-1998; 98US-0096773.  
 PR 17-AUG-1998; 98US-0096891.  
 PR 17-AUG-1998; 98US-0096894.  
 PR 17-AUG-1998; 98US-0096895.  
 PR 17-AUG-1998; 98US-0096897.  
 PR 18-AUG-1998; 98US-0096949.  
 PR 18-AUG-1998; 98US-0096950.  
 PR 18-AUG-1998; 98US-0096959.  
 PR 18-AUG-1998; 98US-0096960.  
 PR 18-AUG-1998; 98US-0097022.  
 PR 19-AUG-1998; 98US-0097141.  
 PR 20-AUG-1998; 98US-0097218.  
 PR 24-AUG-1998; 98US-0097661.  
 PR 26-AUG-1998; 98US-0097951.  
 PR 26-AUG-1998; 98US-0097952.  
 PR 26-AUG-1998; 98US-0097954.  
 PR 26-AUG-1998; 98US-0097955.  
 PR 26-AUG-1998; 98US-0097971.  
 PR 26-AUG-1998; 98US-0097974.  
 PR 26-AUG-1998; 98US-0097978.  
 PR 26-AUG-1998; 98US-0097979.  
 PR 26-AUG-1998; 98US-0097986.  
 PR 26-AUG-1998; 98US-0098014.  
 PR 31-AUG-1998; 98US-0098525.  
 PR 16-SEP-1998; 98US-0100633.  
 PR 12-JAN-1999; 99US-0115565.  
 (GENTH ) GENENTECH INC.  
 Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
 Wood WI, Yuan J;  
 WPI, 2000-072883/06.  
 P-PSDB; AAY66694.  
 Membrane-bound proteins and related nucleotide sequences -  
 Claim 2; Fig 156; 822pp; English.  
 The invention provides membrane-bound PRO polypeptides and  
 polynucleotides encoding them. The PRO sequences of the invention were  
 identified based on extracellular domain homology screening. The PRO  
 sequences have homology with proteins including LDL receptors, TIR  
 ligands and various enzymes. The membrane-bound proteins and receptor  
 molecules are useful as pharmaceutical and diagnostic agents. Receptor  
 immunoadhesins, for instance, can be used as therapeutic agents to block  
 receptor-ligand interactions. The membrane-bound proteins can also be  
 employed for screening of potential peptide or small molecule inhibitors  
 of the relevant receptor/ligand interaction. The PRO encoding sequences  
 are useful as hybridization probes, in chromosome and gene mapping and in  
 the generation of antisense RNA and DNA. PRO nucleic acid sequences  
 will also be useful for the preparation of PRO polypeptides, especially

CC by recombinant techniques.  
 XX SQ Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;  
 Query Match 92.8%; Score 2171.8; DB 21; Length 2185;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 2176; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 Oy 159 GTTCTCTTCCGAGCCAAATCCAGGCGATGTGTGAATTATGAACGTGCCACACATGA 218  
 1 GTTCTCTTCCGAGCCAAATCCAGGCGATGTGTGAATTATGAACGTGCCACACATGA 60  
 Oy 219 AGCTCTGTGACAGTAACTGTGACCAACACACCTGGAATGCCATCTGTCTCCGTTG 278  
 61 AGCTCTGTGACAGTAACTGTGACCAACACACCTGGAATGCCATCTGTCTCCGTTG 120  
 Oy 279 TCTACTTCACGGCGCAAGTGTGATTTGTGTGACGACATGCTGTCCGCTCAGCG 338  
 121 TCTACTTCACGGCGCAAGTGTGATTTGTGTGACGACATGCTGTCCGCTCAGCG 180  
 Oy 339 GGGCCCGAAGATGCCCTCCGCTGCTGTGACATTAACGATTGACGAAGTGTGTGA 398  
 181 GGGCCCGAAGATGCCCTCCGCTGCTGTGACATTAACGATTGACGAAGTGTGTGA 240  
 Oy 399 CGCGCCGGGGCTCTCCGAGGTCCGAGGGTATTCCTCGAACAACCCGGTACCTCAAC 458  
 241 CGCGCCGGGGCTCTCCGAGGTCCGAGGGTATTCCTCGAACAACCCGGTACCTCAAC 300  
 Oy 459 TCATGAGAAACATCATCATCATGATTCAGAGCGGACACCTTCGACACCACTGTG 518  
 301 TCATGAGAAACATCATCATCATGATTCAGAGCGGACACCTTCGACACCACTGTG 360  
 Oy 519 AGGTCTGTGACGTGGGACGAACTCCATCCGCGCATTAAGTGTGGGGCTTCAACGCC 578  
 361 AGGTCTGTGACGTGGGACGAACTCCATCCGCGCATTAAGTGTGGGGCTTCAACGCC 420  
 Oy 579 TGCGCAGGCTCAGACCCCTGGAGCTGTGCAACATCTGGCTGACATCCCTGACGGGG 638  
 421 TGCGCAGGCTCAGACCCCTGGAGCTGTGCAACATCTGGCTGACATCCCTGACGGGG 480  
 Oy 639 CTTTGAATACCTGTCCAGCTGCGGAGCTGTGCTTCGCAACACCCCATTCGAAGCA 698  
 481 CTTTGAATACCTGTCCAGCTGCGGAGCTGTGCTTCGCAACACCCCATTCGAAGCA 540  
 Oy 699 TCCCTCTTACGCTTCAACCGGGTGCCTCTCTCATGCGCTGTGACTTGGGGAGCTCA 758  
 541 TCCCTCTTACGCTTCAACCGGGTGCCTCTCTCATGCGCTGTGACTTGGGGAGCTCA 600  
 Oy 759 AGAGCTGAGTATCTCTGAGGGAGCTTTGAGGGGCTGTCAACTCAAGTATCTGA 818  
 601 AGAGCTGAGTATCTCTGAGGGAGCTTTGAGGGGCTGTCAACTCAAGTATCTGA 660  
 Oy 819 ACTTGGCATGTGCAACATTAAGACATGCGCAATCTCACCCCTGTGTGGGCTGAGG 878  
 661 ACTTGGCATGTGCAACATTAAGACATGCGCAATCTCACCCCTGTGTGGGCTGAGG 720  
 Oy 879 AGCTGAGATGTCAAGGACACCTTCCCTGATGAGGCTGTGCTCTTCATGCGCTGA 938  
 721 AGCTGAGATGTCAAGGACACCTTCCCTGATGAGGCTGTGCTCTTCATGCGCTGA 780  
 Oy 939 GTCCTCCCAAGAGCTGTGGGTCAATGAACATCAAGGCTGATGAGGGAATGCTT 998  
 781 GTCCTCCCAAGAGCTGTGGGTCAATGAACATCAAGGCTGATGAGGGAATGCTT 840  
 Oy 999 TTGACGGGCTGCTTCACTTGTGAACTCACTTGGCCCAATTAACCTCTCTTTG 1058  
 841 TTGACGGGCTGCTTCACTTGTGAACTCACTTGGCCCAATTAACCTCTCTTTG 900  
 Oy 1059 CCATGACCTTTTACCCCGGTGAGTACTGTGTGAGTGTGATCTACACCAACCTT 1118  
 901 CCATGACCTTTTACCCCGGTGAGTACTGTGTGAGTGTGATCTACACCAACCTT 960  
 Oy 1119 GAAACTGTGATTTGATCATTTGTGCTGACCTGTGCTTCAGAGATATATACCA 1178

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Db      1021  ATTCCACTGCTGTGTGGCCGCTGTATGCTCCATGACATGTGAGAGCCGCTACCTGTGG 1080
Qy      1239  AGGTGACCAAGGCGCTCTTCCAGTGTGCTGCGCCCTTCATCATGTGAGACCACTCGAGAC 1298
Db      1081  AGGTGACCAAGGCGCTCTTCCAGTGTGCTGCGCCCTTCATCATGTGAGACCACTCGAGAC 1140
Qy      1299  TCACATTTCTGAGGGTGTGAGTGGAGAACTTAAAGTGTGGAATCTCCCTATGTCTCCG 1358
Db      1141  TCACATTTCTGAGGGTGTGAGTGGAGAACTTAAAGTGTGGAATCTCCCTATGTCTCCG 1200
Qy      1359  TGAAGTGTGTGCTGCGCAATGTGGACAGTCTGACGCAAGCTCCCGCAACCAAGATCT 1418
Db      1201  TGAAGTGTGTGCTGCGCAATGTGGACAGTCTGACGCAAGCTCCCGCAACCAAGATCT 1260
Qy      1419  CTGTCTCTCAAGCGGCACTTTGAATCTTTCCAGTGTGCTTCCAGACACTGSGGATGT 1478
Db      1261  CTGTCTCTCAAGCGGCACTTTGAATCTTTCCAGTGTGCTTCCAGACACTGSGGATGT 1320
Qy      1479  ACACATGATGAGGACCAATGTGTGAGGCACTCCAGCGCTCGGCTTACCTCAATGGGA 1538
Db      1321  ACACATGATGAGTGAACCAATGTGTGAGGCACTCCAGCGCTCGGCTTACCTCAATGTGA 1380
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Db      1381  GCACGGCTGAGCTTAAACCTTCAACTACAGTCTTCCACCAAGAGAGAGAGAGACCA 1440
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Db      1501  GTTACCAAGCCGGCATATACCACTTACCAAGGCTCTCAATTCAGACTGCGGCA 1560
Qy      1719  AGCAGGTGCGAGTACCCCGAGACACCACTGACCAAGATGTGACACAGCTGTGTAAG 1778
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Db      1621  TCATGAGACCAACAAGATCATTTGGTGTGTGGCACTGACTGTGAGTGGCG 1680
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Db      1681  CCATGTTGATGTCTTCTATAAACTTCGTAAAGCGGACACGAGCGGAGTACATCAG 1740
Qy      1899  CGGCGCGGACCTGTGAGATATCCAGGTGTGAGAGAAATCTCCAGACAGAAATCCGAG 1958
Db      1741  CGGCGCGGACCTGTGAGATATCCAGGTGTGAGAGAAATCTCCAGACAGAAATCCGAG 1800
Qy      1959  CAGCAACAGCAGCTCGTCCGGTGTATCAGTGAAGGGGCAATGAGTCCCAACAATTC 2018
Db      1801  CAGCAACAGCAGCTCGTCCGGTGTATCAGTGAAGGGGCAATGAGTCCCAACAATTC 1860
Qy      2019  ATGACCATATTAATTAACAACACTTAACAACAGCAGCATGTGGGCGCACTGAGACAGAAA 2078
Db      1861  ATGACCATATTAATTAACAACACTTAACAACAGCAGCATGTGGGCGCACTGAGACAGAAA 1920
Qy      2079  GCTTGGGGAACCTCTGTGACCCCAAGTACACATATCTCTAAGCTTATATTAATTCAGA 2138
Db      1921  GCTTGGGGAACCTCTGTGACCCCAAGTACACATATCTCTAAGCTTATATTAATTCAGA 1980
Qy      2139  CCCATACCAAGGACAGGTACAGAAACTCAATATGATCCCTCCCAAAAAAATTA 2198
Db      1981  CCCATACCAAGGACAGGTACAGAAACTCAATATGATCCCTCCCAAAAAAATTA 2040
Qy      2199  TAAAAATGCAATGAATGACACAAAGACAGCAACTTTTGTATAGATGGGAGAGACTTT 2258

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Db      2041  TAAATGCAATAGATGACACAAAGACGCACTTTGTATAGATGGGAGAGACTTT 2100
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Db      2101  TTCTGTATATGCTTATATATTAAGTCAATGGGCTGGTTAAAAAACAAGATTAATTA 2160
Qy      2319  AATTTAAAGCAAAAAGTCAAAA 2341
Db      2161  AATTTAAAGCAAAAAGTCAAAA 2183

RESULT 6
AAS21462
ID AAS21462 standard; cDNA; 2185 BP.
XX
AC AAS21462;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human cDNA sequence encoding for PRO1111 polypeptide.
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW adipocyte; A-peptide; factor VIIa; gene therapy; ss.
OS Homo sapiens.
XX
FN WO200140466-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US32678.
XX
PR 01-DEC-1999; 99WO-US28301.
XX
PR 01-DEC-1999; 99WO-US28634.
XX
PR 02-DEC-1999; 99WO-US28551.
XX
PR 02-DEC-1999; 99WO-US28564.
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PR 02-DEC-1999; 99WO-US28565.
XX
PR 09-DEC-1999; 98US-0170262.
XX
PR 16-DEC-1999; 99WO-US30095.
XX
PR 20-DEC-1999; 99WO-US30911.
XX
PR 20-DEC-1999; 99WO-US30999.
XX
PR 30-DEC-1999; 99WO-US31243.
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PR 06-JAN-2000; 2000WO-US00277.
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PR 06-JAN-2000; 2000WO-US00376.
XX
PR 11-FEB-2000; 2000WO-US03565.
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PR 18-FEB-2000; 2000WO-US04341.
XX
PR 18-FEB-2000; 2000WO-US04342.
XX
PR 22-FEB-2000; 2000WO-US04414.
XX
PR 24-FEB-2000; 2000WO-US04914.
XX
PR 24-FEB-2000; 2000WO-US05004.
XX
PR 01-MAR-2000; 2000WO-US05601.
XX
PR 20-MAR-2000; 2000WO-US07377.
XX
PR 21-MAR-2000; 2000WO-US07532.
XX
PR 30-MAR-2000; 2000WO-US08439.
XX
PR 17-MAY-2000; 2000WO-US13705.
XX
PR 22-MAY-2000; 2000WO-US14042.
XX
PR 30-MAY-2000; 2000WO-US14941.
XX
PR 02-JUN-2000; 2000WO-US15264.
XX
PR 10-NOV-2000; 2000WO-US30873.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W,
PI Gerlitsen ME, Goddard A, Godowski PJ, Gurney AU, Sherwood S,
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WJ, Zhang Z;
XX
DR MPI. 2001-408281/43.
XX
DR P-PSDB; AAU12390.
XX
PT Isolated, secretory and transmembrane PRO polypeptide used to detect
other PRO polypeptides, link bioactive molecules to cells expressing

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Db 361 AGGCTCTGCACTTGGGCGAGCACTCCAGGAGTTGAGGTGGGGCTTCAACGGCC 420  
 Qy 579 TGGCAGCCTCAGCAGCCTGGAGCTGTTCGAACAATGGCTGACATCCTTACGGGG 638  
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 Qy 1959 CAGCAACAGAGCTCCGCTCCGCTGTATCAGGTGAAGGGGAGATAGTCTGCCCAATTC 2018  
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 Qy 2139 CCCATACCAAGACAGATACAGAACTCAATATGATCTCCCTCCCAAAACTTGA 2198  
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 Qy 2259 TTCTTGTATATGCTTATATATTAAGTCTATGGCTGTGTAAAAAAACAGATTATATTA 2318  
 Db 2101 TTCTTGTATATGCTTATATATTAAGTCTATGGCTGTGTAAAAAAACAGATTATATTA 2160  
 Qy 2319 AATTTAAAGCAAAAAGTCAAAA 2341  
 Db 2161 AATTTAAAGCAAAAAGTCAAAA 2183

RESULT 8  
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 ID ACA03821 standard; cDNA; 2185 BP.  
 XX  
 AC ACA03821;  
 XX  
 DT 23-MAY-2003 (first entry)  
 XX  
 DE cDNA encoding human PRO polypeptide #219.  
 XX  
 KW Human; PRO polypeptide; secreted and transmembrane protein;  
 KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;  
 KW differentiation; chondrocyte; tumour; genetic disorder;  
 KW cytosolic; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003036180-A1.  
 XX  
 PD 20-FEB-2003.  
 XX  
 PF 09-MAY-2002; 2002US-0143114.  
 XX



PR 31-MAR-1997; 97WO-US05230.  
 PR 12-JUN-1998; 98WO-US14556.  
 PR 14-JUL-1998; 98WO-US14552.  
 PR 28-AUG-1998; 98WO-US17888.  
 PR 10-SEP-1998; 98WO-US18824.  
 PR 14-SEP-1998; 98WO-US19093.  
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 PR 14-SEP-1998; 98WO-US19177.  
 PR 16-SEP-1998; 98WO-US19330.  
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 PR 07-OCT-1998; 98WO-US21141.  
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 PR 29-OCT-1998; 98WO-US22992.  
 PR 20-NOV-1998; 98WO-US24855.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 05-JAN-1999; 99WO-US00106.  
 PR 08-MAR-1999; 99WO-US05028.  
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 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 13-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 05-OCT-1999; 99WO-US21547.  
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 PR 05-JAN-2000; 2000WO-US00219.  
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 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
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 PR 02-MAR-2000; 2000WO-US05746.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 10-MAR-2000; 2000WO-US06319.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08339.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 11-AUG-2000; 2000WO-US22031.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23528.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 25-MAY-2001; 2001WO-US17092.

PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 22-JUN-2001; 2001WO-US20116.  
 PR 29-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 PR 20-DEC-2000; 2000WO-US77259.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 18-MAY-2001; 2001US-0860216.  
 PR 25-MAY-2001; 2001US-086028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 01-JUN-2001; 2001US-0872035.  
 PR 05-JUN-2001; 2001US-0874503.  
 PR 14-JUN-2001; 2001US-0882636.  
 PR 19-JUN-2001; 2001US-0886342.  
 PR 21-JUN-2001; 2001US-0887879.  
 PR 18-JUL-2001; 2001US-0908837.  
 PR 06-AUG-2001; 2001US-0924419.  
 PR 09-AUG-2001; 2001US-0927796.  
 PR 16-AUG-2001; 2001US-0931836.  
 PR 19-DEC-2001; 2001US-0028072.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,  
 PI Gerlitsen ME, Goddard A, Godowski PJ, Gurney AV, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR MPI: 2003-332040/31.  
 DR P-PSDB; AB066788.  
 XX  
 PT New secreted and transmembrane PRO nucleic acids, useful for gene  
 PT therapy, in chromosome and gene mapping, as chromosome markers, in  
 PT tissue typing, and in chromosome identification -  
 XX  
 PS  
 XX  
 YY Claim 2; Fig 437; 660bp; English.  
 XX  
 CC The present invention relates to the isolation of novel human PRO  
 CC polypeptides, and the polynucleotide sequences encoding them. The  
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO  
 CC polypeptides are useful for detecting other PRO polypeptides, for  
 CC linking bioactive molecules to cells expressing PRO polypeptides,  
 CC for modulating biological activities of cells expressing PRO  
 CC polypeptides, and for identifying agonists or antagonists.  
 CC The PRO polypeptides are useful for stimulating the release of  
 CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating  
 CC the proliferation or differentiation of chondrocytes, and detecting the  
 CC presence of tumours. The polynucleotide sequences encoding PRO  
 CC polypeptides are useful as hybridisation probes, in chromosome and  
 CC gene mapping, in the generation of antisense RNA and DNA, in the  
 CC preparation of PRO polypeptides, for generating transgenic animals or  
 CC knockout animals, for the genetic analysis of individuals with genetic  
 CC disorders, and in gene therapy. ACN03603-ACN03877 represent cDNAs  
 CC encoding the human PRO polypeptides of the invention.  
 CC Note: The sequence data for this patent was obtained in electronic  
 CC format directly from the USPTO web site at  
 CC seqdata.uspto.gov/patidentdentry.html.  
 XX  
 SQ Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;  
 Query Match 92.8%; Score 2171.8; DB 25; Length 2185;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 2176; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 QY 159 GTTCTCCTTTCCGAGCCAAATCCAGGCGATGTGATTTATGACGTCACACCATGA 218  
 DB 1 GTTCTCCTTTCCGAGCCAAATCCAGGCGATGTGATTTATGACGTCACACCATGA 60



QY 219 AGCTTTGTGAGAGTAACTGTGACACCAACCTGGAAATGCATCTGCTCCGTTTCG 278  
 Db 61 AGCTTTGTGAGAGTAACTGTGACACCAACCTGGAAATGCATCTGCTCCGTTTCG 120  
 QY 279 TCTAATCTCAAGGCGCAAGTGTGATTTCTGTGTGACAGCATGTGCTGTGCTGACGCG 338  
 Db 121 TCTAATCTCAAGGCGCAAGTGTGATTTCTGTGTGACAGCATGTGCTGTGCTGACGCG 180  
 QY 339 GAGCCCAAGAACTGCGCCCTCCGTCGTGTGACAGTAAACCAATTGACGAAGGTGGTGTGA 398  
 Db 181 GAGCCCAAGAACTGCGCCCTCCGTCGTGTGACAGTAAACCAATTGACGAAGGTGGTGTGA 240  
 QY 399 CGCGCCGCGGCTCTCCGAGGTCCCGAGAGGTATTCCTCGAACAACCGGATACCTCAAC 458  
 Db 241 CGCGCCGCGGCTCTCCGAGGTCCCGAGAGGTATTCCTCGAACAACCGGATACCTCAAC 300  
 QY 459 TCAATGAGAAACAATCCAGATGATCCAGGCGGACACTTTCGCACTCTCAACCACTGG 518  
 Db 301 TCAATGAGAAACAATCCAGATGATCCAGGCGGACACTTTCGCACTCTCAACCACTGG 360  
 QY 519 AGGTCTGAGAGTGGGAGAGAACTCCATCCGAGATTGAGTGGGGGCTTCAACGAGCC 578  
 Db 361 AGGTCTGAGAGTGGGAGAGAACTCCATCCGAGATTGAGTGGGGGCTTCAACGAGCC 420  
 QY 579 TGCGCAAGCTCAGACACCTGAGAGCTGTTGACAACTGCTGACAGTCACTCCCTAGCGGG 638  
 Db 421 TGCGCAAGCTCAGACACCTGAGAGCTGTTGACAACTGCTGACAGTCACTCCCTAGCGGG 480  
 QY 639 CTTTGAATTAATCTGTCAGAGCTGCGGAGCTGTGCTTGGCAACAACCCCATCGAAAGCA 698  
 Db 481 CTTTGAATTAATCTGTCAGAGCTGCGGAGCTGTGCTTGGCAACAACCCCATCGAAAGCA 540  
 QY 699 TCCCTCTTACGAGCTTCAACCGGAGGCTCCCTCATGCGGCTGGACCTTGGGGAGAGCTCA 758  
 Db 541 TCCCTCTTACGAGCTTCAACCGGAGGCTCCCTCATGCGGCTGGACCTTGGGGAGAGCTCA 600  
 QY 759 AGAAGCTGAGATATATCTGTAGGAGAGCTTTTGAAGGGGCTTCAACCTCAAGTATCTGA 818  
 Db 601 AGAAGCTGAGATATATCTGTAGGAGAGCTTTTGAAGGGGCTTCAACCTCAAGTATCTGA 660  
 QY 819 ACTTGGGAGTGTGCAATTAAGAATGCCAATCTCAACCCCTGTGTGGGCTGAGAG 878  
 Db 661 ACTTGGGAGTGTGCAATTAAGAATGCCAATCTCAACCCCTGTGTGGGCTGAGAG 720  
 QY 879 AGCTGAGATGTGAGGAGACCACTCCCTGAGATCAGGCTGTGCTTCCATGAGCTGGA 938  
 Db 721 AGCTGAGATGTGAGGAGACCACTCCCTGAGATCAGGCTGTGCTTCCATGAGCTGGA 780  
 QY 939 GCTCCCTCAAGAACTGTGAGTCACTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 998  
 Db 781 GCTCCCTCAAGAACTGTGAGTCACTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 840  
 QY 999 TTGACGAGGCTGCTTCACTTGTGAACTCACTTGGCCCAATTAACCTCTCTTCTTTCG 1058  
 Db 841 TTGACGAGGCTGCTTCACTTGTGAACTCACTTGGCCCAATTAACCTCTCTTCTTTCG 900  
 QY 1059 CCCATGAGCTCTTAAACCCCGGTGAGATACCTGTGTGAGATTTGACACCAACCTT 1118  
 Db 901 CCCATGAGCTCTTAAACCCCGGTGAGATACCTGTGTGAGATTTGACACCAACCTT 960  
 QY 1119 GGAATGATGATGACATTTCTGTGCTAGCTGAGTGGCTTCAAGAGATTAATACCAACA 1178  
 Db 961 GGAATGATGATGACATTTCTGTGCTAGCTGAGTGGCTTCAAGAGATTAATACCAACA 1020  
 QY 1179 ATTTCACCTGTGTGCGCTGTGATGCTCCCATGACATGCGAGCGGCTACCTGCTGG 1238  
 Db 1021 ATTTCACCTGTGTGCGCTGTGATGCTCCCATGACATGCGAGCGGCTACCTGCTGG 1080  
 QY 1239 AGGTGAGCAGGCGCTCTCCAGTGTGCTGCGCCCTTCAATGAGAGCAGCAGCAGCAGC 1298  
 Db 1081 AGGTGAGCAGGCGCTCTCTTCAAGTGTGCTGCGCCCTTCAATGAGAGCAGCAGCAGCAGC 1140  
 QY 1299 TCAACATTTCTGAGGGGTGAGTGCAGAACTTAAGTGTGAGTCTCCCTATGTCTCCG 1358

Db 1141 TCAACATTTCTGAGGGGTGAGTGCAGAACTTAAGTGTGAGTCTCCCTATGTCTCCG 1200  
 QY 1359 TGAAGTGTGTGCTGCCCAATGAGGACAGTGTCTAGCCACGCTCCCGACCAAGATCT 1418  
 Db 1201 TGAAGTGTGTGCTGCCCAATGAGGACAGTGTCTAGCCACGCTCCCGACCAAGATCT 1260  
 QY 1419 CTGTCTCTCAAGCAGGCGCACTTGAACCTTTCCACGAGTGTCTTTCAGACCTGGGGGT 1478  
 Db 1261 CTGTCTCTCAAGCAGGCGCACTTGAACCTTTCCACGAGTGTCTTTCAGACCTGGGGGT 1320  
 QY 1479 ACAATGATGAGGAGCAATGTTGACAGCACTTCCAAAGCTGTGCTTACCTCAATGGA 1538  
 Db 1321 ACAATGATGAGGAGCAATGTTGACAGCACTTCCAAAGCTGTGCTTACCTCAATGGA 1380  
 QY 1539 GCACGCTGAGCTTAAACCTTCAACAGCTTCTTCAACCAAGAGAGAGAGAGCA 1598  
 Db 1381 GCACGCTGAGCTTAAACCTTCAACAGCTTCTTCAACCAAGAGAGAGAGAGCA 1440  
 QY 1599 CGAGATCTGCGCTGAGAGACCAACGAGAAAGTACAAAGCTGTTCCTACCAAGCTCACTG 1658  
 Db 1441 CGAGATCTGCGCTGAGAGACCAACGAGAAAGTACAAAGCTGTTCCTACCAAGCTCACTG 1500  
 QY 1659 GTTACAGCGGAGATATACCACTCTACAGAGTGTCTCATTTCAAGTACCTCCGTGTGCGCA 1718  
 Db 1501 GTTACAGCGGAGATATACCACTCTACAGAGTGTCTCATTTCAAGTACCTCCGTGTGCGCA 1560  
 QY 1719 AGCAGGTGAGATACCCGCGACAGACCACTGACAAATGACAGACAGCCTGATGAG 1778  
 Db 1561 AGCAGGTGAGATACCCGCGACAGACCACTGACAAATGACAGACAGCCTGATGAG 1620  
 QY 1779 TCAATGAGACCAACCAATATCATCTGCTGTGTGAGAGTACCTGCTGCTGCTGCTGCTG 1838  
 Db 1621 TCAATGAGACCAACCAATATCATCTGCTGTGTGAGAGTACCTGCTGCTGCTGCTGCTGCTG 1680  
 QY 1839 CCAATGATGATGCTTCTTATTAACCTTGTGAGGAGCAGCAGAGCGAGTACAGTCAAG 1898  
 Db 1681 CCAATGATGATGCTTCTTATTAACCTTGTGAGGAGCAGCAGAGCGAGTACAGTCAAG 1740  
 QY 1899 CCGCGCGGAGCTGTTGAGATATCCAGGTGAGAGAGATCCAGACAGCAATCCGAG 1958  
 Db 1741 CCGCGCGGAGCTGTTGAGATATCCAGGTGAGAGAGATCCAGACAGCAATCCGAG 1800  
 QY 1959 CAGCAAGAGAGCTCCCTCCGCTGATCAGTGAAGGGGAGAGTATGCTGCCCAATTC 2018  
 Db 1801 CAGCAAGAGAGCTCCCTCCGCTGATCAGTGAAGGGGAGAGTATGCTGCCCAATTC 1860  
 QY 2019 ATGACATATTAATCAACCACTTCAACCAAGCACTGAGGAGCCCACTGACAGAAACA 2078  
 Db 1861 ATGACATATTAATCAACCACTTCAACCAAGCACTGAGGAGCCCACTGACAGAAACA 1920  
 QY 2079 GCTGAGGAGAACTCTGTGACACCCCAAGTCAACCTATCTGTGAACCTTATATTAATGAGA 2138  
 Db 1921 GCTGAGGAGAACTCTGTGACACCCCAAGTCAACCTATCTGTGAACCTTATATTAATGAGA 1980  
 QY 2139 CCCATACCAAGAGACAGTACAGGAACTCAATATGATCTCCCTCCCGCAAAAACCTTA 2198  
 Db 1981 CCCATACCAAGAGACAGTACAGGAACTCAATATGATCTCCCTCCCGCAAAAACCTTA 2040  
 QY 2199 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2258  
 Db 2041 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2100  
 QY 2259 TTTCTGATATGCTTATATATTAATTAAGTATGAGTGTGATGATGATGATGATGATGATGAT 2318  
 Db 2101 TTTCTGATATGCTTATATATTAATTAAGTATGAGTGTGATGATGATGATGATGATGATGAT 2160  
 QY 2319 AATTTAAGCAAAAAGTCAAAA 2341  
 Db 2161 AATTTAAGCAAAAAGTCAAAA 2183

ACA04242  
 ID ACA04242 standard; cDNA; 2185 BP.  
 AC ACA04242;  
 DT 27-MAY-2003 (first entry)  
 XX  
 DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 437.  
 XX  
 KW Human; ss; gene; secreted protein; transmembrane protein; PRO;  
 KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;  
 KW infertility; birth defects; premature aging; AIDS; biosensor;  
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;  
 KW bioeffector; tumour.  
 XX  
 OS Homo sapiens.  
 EN US2003032155-A1.  
 XX  
 PD 13-FEB-2003.  
 XX  
 PF 03-MAY-2002; 2002US-0137865.  
 XX  
 PR 31-MAR-1997; 97WO-US05230.  
 PR 12-JUN-1998; 98WO-US12456.  
 PR 14-JUL-1998; 98WO-US14552.  
 PR 28-AUG-1998; 98WO-US17888.  
 PR 10-SEP-1998; 98WO-US18824.  
 PR 14-SEP-1998; 98WO-US18093.  
 PR 14-SEP-1998; 98WO-US19094.  
 PR 14-SEP-1998; 98WO-US19177.  
 PR 16-SEP-1998; 98WO-US19330.  
 PR 17-SEP-1998; 98WO-US19437.  
 PR 07-OCT-1998; 98WO-US21141.  
 PR 29-OCT-1998; 98WO-US22991.  
 PR 29-OCT-1998; 98WO-US22992.  
 PR 20-NOV-1998; 98WO-US24855.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 05-JAN-1999; 99WO-US00106.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 10-MAR-1999; 99WO-US05190.  
 PR 20-APR-1999; 99WO-US06615.  
 PR 14-MAY-1999; 99WO-US10733.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 13-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 29-NOV-1999; 99WO-US28214.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 02-DEC-1999; 99WO-US28651.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 22-DEC-1999; 99WO-US30999.  
 PR 30-DEC-1999; 99WO-US31720.  
 PR 30-DEC-1999; 99WO-US31243.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 11-FEB-2000; 2000WO-US00376.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.

PR 01-MAR-2000; 2000WO-US05601.  
 PR 02-MAR-2000; 2000WO-US05746.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 10-MAR-2000; 2000WO-US06319.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 11-AUG-2000; 2000WO-US22031.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 22-JUN-2001; 2001WO-US20116.  
 PR 29-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 18-MAY-2001; 2001US-0860216.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 01-JUN-2001; 2001US-0872035.  
 PR 05-JUN-2001; 2001US-0874503.  
 PR 14-JUN-2001; 2001US-0882636.  
 PR 19-JUN-2001; 2001US-0886342.  
 PR 21-JUN-2001; 2001US-0887879.  
 PR 18-JUL-2001; 2001US-0908827.  
 PR 06-AUG-2001; 2001US-0924419.  
 PR 09-AUG-2001; 2001US-0927796.  
 PR 16-AUG-2001; 2001US-0931836.  
 PR 19-DEC-2001; 2001US-0028072.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,  
 PI Gerlitsen ME, Goddard A, Godowski PJ, Gurney AJ, Sherwood S,  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR MPI; 2003-331925/31.  
 DR P-ESDB; ABU67064.  
 XX  
 PT New secreted and transmembrane nucleic acids and polypeptides,  
 PT designated as PRO, useful for treating inflammation, organ failure,  
 PT atherosclerosis, cardiac injury, infertility, birth defects, premature  
 PT aging, AIDS, or cancer  
 XX  
 PS Claim 2; Fig 437; 659p; English.  
 XX  
 CC The invention relates to an isolated nucleic acid comprising, or which is  
 CC at least 80% identical to, or the full-length coding sequence of, any of  
 CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide  
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid  
 CC further comprises the full-length coding sequence of the DNA deposited  
 CC under American Type Culture Collection (ATCC) accession number in a list  
 CC given in the specification. Also included are vectors and host

CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO  
 CC antibodies, PRO extracellular domains and mature sequences, methods  
 CC of detecting PRO proteins, methods for stimulating the release of  
 CC TNF-alpha (tumour necrosis factor alpha) from human blood,  
 CC (and the proliferation of differentiation of chondrocyte cells, the  
 CC proliferation of, or gene expression in pericyte cells, the release or  
 CC proteoglycans from cartilage, proliferation of inner ear utricular  
 CC supporting cells, the proliferation of T-lymphocyte cells, the release  
 CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the  
 CC proliferation of endothelial cells), a method for modulating the uptake  
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells,  
 CC a method for inhibiting the binding of A-peptide to factor VIIa,  
 CC or the differentiation of adipocyte cells, a method for detecting the  
 CC presence of a tumour in a mammal and an oligonucleotide probe derived  
 CC from any of the nucleotide sequences cited above. The nucleic acids and  
 CC polypeptides are useful for treating inflammatory diseases, organ  
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,  
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or  
 CC diabetic complications. The nucleic acids are useful as hybridisation  
 CC probes, in chromosome and gene mapping, and in generating antisense RNA  
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,  
 CC biosensors or bioreactors. Both are useful in tissue typing.  
 CC The present sequence encodes a PRO protein of the invention.  
 CC  
 XX  
 SQ Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;

Query Match 92.8%; Score 2171.8; DB 25; Length 2185;  
 Best Local Similarity 99.7%; Pred. No. 0; Mismatches 7; Indels 0; Gaps 0;  
 Matches 2176; Conservative 0; Nismatches 7; Indels 0; Gaps 0;

QY 159 GTTCTCTTTCCGAGCCAAATCCAGGCGATGTGATTAATGAACGTCACACCATGA 218  
 Db 1 GTTCTCTTTCCGAGCCAAATCCAGGCGATGTGATTAATGAACGTCACACCATGA 60  
 QY 219 AGCTTTGTGGCAGGTAATCTGTGCACACCACTGGAATGCCATCTCTCCGTTG 278  
 Db 61 AGCTTTGTGGCAGGTAATCTGTGCACACCACTGGAATGCCATCTCTCCGTTG 120  
 QY 279 TCTACCTACGCGGCGAATGTGATTTCTGTGAGCGCATGCGTCCGCTCAGCG 338  
 Db 121 TCTACCTACGCGGCGAATGTGATTTCTGTGAGCGCATGCGTCCGCTCAGCG 180  
 QY 339 GGGCCGAGAACTGCCCCCTCGCTGCTGTCGATGAACGATTGAGAAAGGTGTGTCA 398  
 Db 181 GGGCCGAGAACTGCCCCCTCGCTGCTGTCGATGAACGATTGAGAAAGGTGTGTCA 240  
 QY 399 CGCGCGGGGCTCTCGAGGTCCCGAGGGTATTCCTCGAACAACCGGTACTCAAC 458  
 Db 241 CGCGCGGGGCTCTCGAGGTCCCGAGGGTATTCCTCGAACAACCGGTACTCAAC 300  
 QY 459 TCATGAGAGAACATCCAGATGATCCAGGCGAACAATTCGCGCACTCCACCACTTGG 518  
 Db 301 TCATGAGAGAACATCCAGATGATCCAGGCGAACAATTCGCGCACTCCACCACTTGG 360  
 QY 519 AGGTCTGCAATGGGAGAGAACTCATCCGAGATTGAGGTGGGGCTTTCAACGCGC 578  
 Db 361 AGGTCTGCAATGGGAGAGAACTCATCCGAGATTGAGGTGGGGCTTTCAACGCGC 420  
 QY 579 TGGCAGCTTACGACCTCTGAGAGCTTTGACAACTGAGCTGATCTCTTACGCGGG 638  
 Db 421 TGGCAGCTTACGACCTCTGAGAGCTTTGACAACTGAGCTGATCTCTTACGCGGG 480  
 QY 639 CCTTTGATTAATCTGTCAGAGCTGCGGAGCTCTGGCTTCGAAACAACCCCATCGAAACA 698  
 Db 481 CCTTTGATTAATCTGTCAGAGCTGCGGAGCTCTGGCTTCGAAACAACCCCATCGAAACA 540  
 QY 699 TCCCTCTTTAGCCCTTCAACCGGGTGCCTCCCTCATGCGCTGAGACTTTGGGGAGCTCA 758  
 Db 541 TCCCTCTTTAGCCCTTCAACCGGGTGCCTCCCTCATGCGCTGAGACTTTGGGGAGCTCA 600  
 QY 759 AGAAGCTGAGATATCTCTGAGGAGCTTTTGAAGGGCTGTTCAACCTCAAGATCTGA 818  
 Db 601 AGAAGCTGAGATATCTCTGAGGAGCTTTTGAAGGGCTGTTCAACCTCAAGATCTGA 660

QY 819 ACTTGGCATGTGCAACATTAAAGACATGCCATCTACCCCCCTGTGGGCTGGAG 878  
 Db 661 ACTTGGCATGTGCAACATTAAAGACATGCCATCTACCCCCCTGTGGGCTGGAG 720  
 QY 879 AGCTGAGATGTCAAGGAAACCACTTCCCTGAGATCAGGCTGCTCTTCCATGCTGA 938  
 Db 721 AGCTGAGATGTCAAGGAAACCACTTCCCTGAGATCAGGCTGCTCTTCCATGCTGA 780  
 QY 939 GCTCCCTCAAGAACTCTGGGTCTATGAACTCAGAGTCAAGCTGATGAGGGAATGTT 998  
 Db 781 GCTCCCTCAAGAACTCTGGGTCTATGAACTCAGAGTCAAGCTGATGAGGGAATGTT 840  
 QY 999 TTGACGGGCTGCTTCACTTGTGAACTCAATTTGAGCCCAATAAATCTCTTTTGC 1058  
 Db 841 TTGACGGGCTGCTTCACTTGTGAACTCAATTTGAGCCCAATAAATCTCTTTTGC 900  
 QY 1059 CCCATGACCTCTTTTACCCCGCTGAGTAACTGTGAGAGTTGATCTACCAACAACCTT 1118  
 Db 901 CCCATGACCTCTTTTACCCCGCTGAGTAACTGTGAGAGTTGATCTACCAACAACCTT 960  
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 Db 961 GGAATGTGATTTGATGATCTGTGCTAGCTGAGTGGCTTGGAGATTAATACCA 1020  
 QY 1179 ATTCCACTGCTGTGGCCGCTGTATGCTCCATGCAATGCGAGCGCTACCTGTTG 1238  
 Db 1021 ATTCCACTGCTGTGGCCGCTGTATGCTCCATGCAATGCGAGCGCTACCTGTTG 1080  
 QY 1239 AGGTGACACAGGCTCTTCCAGTGTCTGTGCCCCCTTATCANTGAGACGACCTGAGACC 1298  
 Db 1081 AGGTGACACAGGCTCTTCCAGTGTCTGTGCCCCCTTATCANTGAGACGACCTGAGACC 1140  
 QY 1299 TCAACATTTCTGAGAGGTGAGATGAGCACTTAAGTGTGGAATCCCCCTATGTCCTCG 1358  
 Db 1141 TCAACATTTCTGAGAGGTGAGATGAGCACTTAAGTGTGGAATCCCCCTATGTCCTCG 1200  
 QY 1359 TGAAGTGGTGTCTGCCAATGAGCAGNGCTCAGCAGAGCTCCCGCAACCAAGATCT 1418  
 Db 1201 TGAAGTGGTGTCTGCCAATGAGCAGNGCTCAGCAGAGCTCCCGCAACCAAGATCT 1260  
 QY 1419 CTGTCTCAACGAGGAGCACTTGAATTTTCCAGTGTCTTTCAGACACTGGGGTGT 1478  
 Db 1261 CTGTCTCAACGAGGAGCACTTGAATTTTCCAGTGTCTTTCAGACACTGGGGTGT 1320  
 QY 1479 ACAATGATGAGGAGCAATGTTGCAAGCACTCAACGCTCGGCTTCACTCAATGGA 1538  
 Db 1321 ACAATGATGAGGAGCAATGTTGCAAGCACTCAACGCTCGGCTTCACTCAATGGA 1380  
 QY 1539 GCAAGGCTGAGCTTAACACCTCCAACTACAGCTTCTTCAACAGAGAACAGGAGAACCA 1598  
 Db 1381 GCAAGGCTGAGCTTAACACCTCCAACTACAGCTTCTTCAACAGAGAACAGGAGAACCA 1440  
 QY 1599 CGAGATCTCGCTGAGGAGCAACAGCGAAAGTCAAGGCTGTTCTTACACAGTCACTG 1658  
 Db 1441 CGAGATCTCGCTGAGGAGCAACAGCGAAAGTCAAGGCTGTTCTTACACAGTCACTG 1500  
 QY 1659 GTTACCAAGCGGCAATATACACTCTTACACAGGTGCTTCACTCAACCTGTCCTCA 1718  
 Db 1501 GTTACCAAGCGGCAATATACACTCTTACACAGGTGCTTCACTCAACCTGTCCTCA 1560  
 QY 1719 AGCAGGTGAGTACCGGCGAGACACCACTGACAGAGTCAACAGGCTGAGATGAG 1778  
 Db 1561 AGCAGGTGAGTACCGGCGAGACACCACTGACAGAGTCAACAGGCTGAGATGAG 1620  
 QY 1779 TCATGAAGACCAACAGATCATCATTTGAGCTTGTGTGAGTACTGTGTAAGTCCG 1838  
 Db 1621 TCATGAAGACCAACAGATCATCATTTGAGCTTGTGTGAGTACTGTGTAAGTCCG 1680  
 QY 1839 CCATGTTGATTTCTTCTATTAACCTTGTGTAAGCGGACACAGACGAGATCACTCAAG 1898  
 Db 1681 CCATGTTGATTTCTTCTATTAACCTTGTGTAAGCGGACACAGACGAGATCACTCAAG 1740

Qy 1899 CCGCCCGAGCTGTGAGATTAATCCAGGTGAGCAAGAACATCCAGCAGCAATCCGAG 1958  
Db 1741 CCGCCCGAGCTGTGAGATTAATCCAGGTGAGCAAGAACATCCAGCAGCAATCCGAG 1800  
Qy 1959 CAGCAACAGCAGCTCCGCTCCGCTGTATCAAGTGAAGGGGCACTAGTGTCCCAATTC 2018  
Db 1801 CAGCAACAGCAGCTCCGCTCCGCTGTATCAAGTGAAGGGGCACTAGTGTCCCAATTC 1860  
Qy 2019 ATGACCATTTTACTACACAACCTTACAAACAGCAGCATGAGGCCCCAGTGAAGAAAACA 2078  
Db 1861 ATGACCATTTTACTACACAACCTTACAAACAGCAGCATGAGGCCCCAGTGAAGAAAACA 1920  
Qy 2079 GCTTGAGGAACTCTCTGCAACCCGACAGTCCACTATCTGTGAACTTATTAATTGAGA 2138  
Db 1921 GCTTGAGGAACTCTCTGCAACCCGACAGTCCACTATCTGTGAACTTATTAATTGAGA 1980  
Qy 2139 CCCATACCAAGACAGGTAACAGAACTCAAAATATGACTCCCTCCCAAAAACTTA 2198  
Db 1981 CCCATACCAAGACAGGTAACAGAACTCAAAATATGACTCCCTCCCAAAAACTTA 2040  
Qy 2199 TAAATGCAATGATGATGACACACAAAGACAGCACTTTTGTACAGAGTGGGAGACATTT 2258  
Db 2041 TAAATGCAATGATGATGACACACAAAGACAGCACTTTTGTACAGAGTGGGAGACATTT 2100  
Qy 2259 TTCTGTATGATGCTTATATATTAACTTATGAGGCTGTGTTAAAAAACAGATTATTTAA 2318  
Db 2101 TTCTGTATGATGCTTATATATTAACTTATGAGGCTGTGTTAAAAAACAGATTATTTAA 2160  
Qy 2319 AATTTAAAGCAAAAAGTCAAAA 2341  
Db 2161 AATTTAAAGCAAAAAGTCAAAA 2183

## RESULT 10

ID ABX89359 standard; cDNA; 2185 BP.

XX AC ABX89359;

DT 13-MAY-2003 (first entry)

DE DNA encoding novel secreted and transmembrane protein PRO111.

XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumor; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpesiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ss.

XX Homo sapiens.

OS US2003017563-A1.

XX PD 23-JAN-2003.

XX PF 07-MAY-2002; 2002US-0140808.

XX 31-MAR-1997; 97WO-US05230.  
PR 12-JUN-1998; 98WO-US12456.  
PR 14-JUL-1998; 98WO-US14552.  
PR 28-AUG-1998; 98WO-US14888.  
PR 10-SEP-1998; 98WO-US18824.  
PR 14-SEP-1998; 98WO-US19093.  
PR 14-SEP-1998; 98WO-US19094.  
PR 14-SEP-1998; 98WO-US19177.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.

PR 29-OCT-1998; 98WO-US22991.  
PR 29-OCT-1998; 98WO-US22992.  
PR 20-NOV-1998; 98WO-US24855.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 10-MAR-1999; 99WO-US05190.  
PR 20-APR-1999; 99WO-US08615.  
PR 14-MAY-1999; 99WO-US10733.  
PR 02-JUN-1999; 99WO-US12252.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 13-SEP-1999; 99WO-US20944.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
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PR 02-DEC-1999; 99WO-US28554.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 20-DEC-1999; 99WO-US30999.  
PR 22-DEC-1999; 99WO-US30720.  
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PR 06-JAN-2000; 2000WO-US00277.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
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PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
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PR 02-MAR-2000; 2000WO-US05746.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
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PR 02-JUN-2000; 2000WO-US15264.  
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PR 08-NOV-2000; 2000WO-US30952.  
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PR 01-DEC-2000; 2000WO-US32678.  
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PR 20-JUN-2001; 2001WO-US19692.  
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PR 29-JUN-2001; 2001WO-US21066.  
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PR 20-DEC-2000; 2000US-0747259.  
PR 28-FEB-2001; 2001US-0796498.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.

PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 18-MAY-2001; 2001US-0860218.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 01-JUN-2001; 2001US-0872035.  
 PR 05-JUN-2001; 2001US-0874503.  
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 PR 18-JUL-2001; 2001US-0908827.  
 PR 06-AUG-2001; 2001US-0924419.  
 PR 09-AUG-2001; 2001US-0927796.  
 PR 16-AUG-2001; 2001US-0931836.  
 PR 19-DEC-2001; 2001US-0028072.  
 XX (GETH ) GENENTECH INC.  
 PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W,  
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX WPI: 2003-148238/14.  
 DR P-PSDB; ABUS9869.  
 XX  
 PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
 PT are therapeutically useful for enhancing immune response and in cancer  
 PT treatments -  
 PS Claim 2; Fig 437; 659p; English.  
 XX  
 CC The invention describes an isolated human PRO polypeptide. The PRO  
 CC polypeptides are useful in detecting human PRO polypeptides in a sample, in  
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
 CC in modulating at least one biological activity of a cell expressing a PRO  
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
 CC stimulate adrenal cortical capillary endothelial growth, and PRO536,  
 CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
 CC useful for treating conditions or disorders where angiogenesis would be  
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
 CC useful for treating cancerous tumors. PRO812 inhibits vascular  
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
 CC cells and is thus useful for inhibiting endothelial cell growth in  
 CC mammals which would be beneficial in inhibiting tumor growth. PRO826,  
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing  
 CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of  
 CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
 CC rod photoreceptor cells) and therefore are useful for treating retinal  
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
 CC and PRO1106 induce proliferation of mammalian kidney mesangial cells,  
 CC and therefore are useful for treating kidney disorders associated with  
 CC decreased mesangial cell function such as Berger disease or other  
 CC nephropathies associated with dermatitis, herpeticiforms or Crohn's  
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
 CC proliferation and/or redifferentiation of chondrocytes in culture and  
 CC are thus useful for treating sports injuries, and arthritis. This  
 CC sequence encodes a novel human PRO protein.  
 XX  
 SQ Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;  
 Query Match 92.8%; Score 2171.8; DB 25; Length 2185;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 2176; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Db 61 AGCTCTGTGGCAGAGTAATCTGTGACACCAACACCTGGAATGACATCTGCTCCGTTTCG 120  
 Qy 279 TCTACCTCAGCGGCGCAGTGTGATCTGTGTGAGGACATGCTGCGCGCCCTCAGCCG 338  
 Db 121 TCTACCTCAGCGGCGCAGTGTGATCTGTGTGAGGACATGCTGCTGCGCCCTCAGCCG 180  
 Qy 339 GGCCTCCAGAACTGCGCCCTCGCTGCTGTGTGACATCAAGTTGAGAGGTGTGTGCA 398  
 Db 181 GGCCTCCAGAACTGCGCCCTCGCTGCTGTGTGACATCAAGTTGAGAGGTGTGTGCA 240  
 Qy 399 GCGCGCGGCGCTCTCGAGGTCCCGAGGGATATTCCTGTGAAACCCCGGTACTCAAC 458  
 Db 241 GCGCGCGGCGCTCTCGAGGTCCCGAGGGATATTCCTGTGAAACCCCGGTACTCAAC 300  
 Qy 459 TCATGAGAAACAAATCATCATGATTCAGGCGCAACCTTCGCGACCTCCACCACTCG 518  
 Db 301 TCATGAGAAACAAATCATCATGATTCAGGCGCAACCTTCGCGACCTCCACCACTCG 360  
 Qy 519 AGTCTCGAGTTGGGAGGAGAACTCCATCCGAGATTGAGTGGGGCTTCAACGAGCC 578  
 Db 361 AGTCTCGAGTTGGGAGGAGAACTCCATCCGAGATTGAGTGGGGCTTCAACGAGCC 420  
 Qy 579 TGCCAGGCTCAGCACCCTGAGGCTGTTCGAACTGCTGACAGTATCCCTAGCGGG 638  
 Db 421 TGCCAGGCTCAGCACCCTGAGGCTGTTCGAACTGCTGACAGTATCCCTAGCGGG 480  
 Qy 639 CCTTTGAATATCTTCCAGTGTGCGGAGCTGTGCTTGTGCAACACCCCATGCAAGCA 698  
 Db 481 CCTTTGAATATCTTCCAGTGTGCGGAGCTGTGCTTGTGCAACACCCCATGCAAGCA 540  
 Qy 699 TCCCTCTTACGCTTCAACCGGGGTGCGCTCCCTCATGCGGCTGGAATTTGGGGAGCTCA 758  
 Db 541 TCCCTCTTACGCTTCAACCGGGGTGCGCTCCCTCATGCGGCTGGAATTTGGGGAGCTCA 600  
 Qy 759 AGAAGCTGAGTATATCTCTGAGGAGCTTTTGAAGGAGCTGTTCACCTCAAGTATCTGA 818  
 Db 601 AGAAGCTGAGTATATCTCTGAGGAGCTTTTGAAGGAGCTGTTCACCTCAAGTATCTGA 660  
 Qy 819 ACTTGGGATGTGCAACATTAAGACATGCCAATCTCACCCCTGTGGGGCTGAGAG 878  
 Db 661 ACTTGGGATGTGCAACATTAAGACATGCCAATCTCACCCCTGTGGGGCTGAGAG 720  
 Qy 879 AGCTGAGATGTGAGGAGCAACCTTCCTGAGATCAGGCGCTCTTCATAGGCGCTGA 938  
 Db 721 AGCTGAGATGTGAGGAGCAACCTTCCTGAGATCAGGCGCTCTTCATAGGCGCTGA 780  
 Qy 939 GCTCCCTCAAGAACTCTGAGGTCAATGAACTCAGAGTCAAGCTTATGAGGAGATGCTT 998  
 Db 781 GCTCCCTCAAGAACTCTGAGGTCAATGAACTCAGAGTCAAGCTTATGAGGAGATGCTT 840  
 Qy 999 TTGACGGGCTGCTTCACTTGTGAACTCACTTGGCCCAATPACTCTCTTCTTTCG 1058  
 Db 841 TTGACGGGCTGCTTCACTTGTGAACTCACTTGGCCCAATPACTCTCTTCTTTCG 900  
 Qy 1059 CCAATGACCTTTTAAACCCCGGTGAGTACCTGTGAGATTGCATCTAACAACAACCTT 1118  
 Db 901 CCAATGACCTTTTAAACCCCGGTGAGTACCTGTGAGATTGCATCTAACAACAACCTT 960  
 Qy 1119 GGAAGTGTGATGTGACATTTGTGTGCTGAGGCTGTGAGTGTGAGATATACCAACA 1178  
 Db 961 GGAAGTGTGATGTGACATTTGTGTGCTGAGGCTGTGAGTGTGAGATATACCAACA 1020  
 Qy 1179 ATTCCACTGTGTGCGCGCTGTCAATGCTCCATGACATGCGAGCGGCTACTCTGTGG 1238  
 Db 1021 ATTCCACTGTGTGCGCGCTGTCAATGCTCCATGACATGCGAGCGGCTACTCTGTGG 1080  
 Qy 1239 AGTGTGACAGGCGCTTCCAGTGTCTGTGCGGCTTCCATATGAGCGCACTGTGAGACC 1298  
 Db 1081 AGTGTGACAGGCGCTTCCAGTGTCTGTGCGGCTTCCATATGAGCGCACTGTGAGACC 1140  
 Qy 1299 TCAACATTTCTGAGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1358

Db 1141 TCACATTTCTGAGGGTCGAGTGGCAAACTTAAGTGTGGAATCCCTTATGTCTCCG 1200  
 Qy 1359 TGAAGTGTGTGCTGCCAAATGGGACAGTGTCAAGCCAGCTCCCGCAGCCAGAGATCT 1418  
 Db 1201 TGAAGTGTGTGCTGCCAAATGGGACAGTGTCTAGCCAGCTCCCGCAGCCAGAGATCT 1260  
 Qy 1419 CTGTCTCAACGACGGCAGCTTGAATTTTCCAGCTGTGCTTTCAGACACTGGGGTGT 1478  
 Db 1261 CTGTCTCAACGACGGCAGCTTGAATTTTCCAGCTGTGCTTTCAGACACTGGGGTGT 1320  
 Qy 1479 ACACATGACATGGGGACCAATGTTGGAGGGAATCCAGCCCTCGGCTTCATCCATGGGA 1538  
 Db 1321 ACACATGACATGGGGACCAATGTTGGAGGGAATCCAGCCCTCGGCTTCATCCATGGGA 1380  
 Qy 1539 GCACGGCTGAGCTTAAACCTCCAACTAGAGCTTCTTCAACAAGAGAGGAGAGCA 1598  
 Db 1381 GCACGGCTGAGCTTAAACCTCCAACTAGAGCTTCTTCAACAAGAGAGAGAGCA 1440  
 Qy 1599 CGAGATCTCGCTGAGGACACACCGGAAAGTACAAGCTGTCTTCAACAGTCCATG 1658  
 Db 1441 CGAGATCTCGCTGAGGACACACCGGAAAGTACAAGCTGTCTTCAACAGTCCATG 1500  
 Qy 1659 GTTACAGCGGAGATATACCACTCTACACAGGTGTCTATTCAGACTACCGGTGCCA 1718  
 Db 1501 GTTACAGCGGAGATATACCACTCTACACAGGTGTCTATTCAGACTACCGGTGCCA 1560  
 Qy 1719 AGCAGGTGCGAGTACCCCGGACAGACCACTGACAGATGACAGCAAGCTGATGAAG 1778  
 Db 1561 AGCAGGTGCGAGTACCCCGGACAGACCACTGACAGATGACAGCAAGCTGATGAAG 1620  
 Qy 1779 TCATGAAGACCAACCAAGATCATTTGGCTGCTTGTGCGAGTGAATCTGTAGCTGCCG 1838  
 Db 1621 TCATGAAGACCAACCAAGATCATTTGGCTGCTTGTGCGAGTGAATCTGTAGCTGCCG 1680  
 Qy 1839 CGATGTGATGTGCTTCTTAACTTCTGTAAGCGGACAGACCGGAGTAAAGTACAGCAG 1898  
 Db 1681 CGATGTGATGTGCTTCTTAACTTCTGTAAGCGGACAGACCGGAGTAAAGTACAGCAG 1740  
 Qy 1899 CCGCCCGGACTGTTGATATTCAGAGTGAAGCGGACAGTCCAGAGCAATCCGCGAG 1958  
 Db 1741 CCGCCCGGACTGTTGATATTCAGAGTGAAGCGGACAGTCCAGAGCAATCCGCGAG 1800  
 Qy 1959 CAGCAACAGCAGCTCCGTCGGGTGATCAGGTGAAGGGGCAAGTGTGCCACAATTC 2018  
 Db 1801 CAGCAACAGCAGCTCCGTCGGGTGATCAGGTGAAGGGGCAAGTGTGCCACAATTC 1860  
 Qy 2019 ATGACCATTTTAACTTAACTCAACCTTAACCAAGCAGATGGGGCCCACTGACAGAAACA 2078  
 Db 1861 ATGACCATTTTAACTTAACTCAACCTTAACCAAGCAGATGGGGCCCACTGACAGAAACA 1920  
 Qy 2079 GCGTGGGGAATCTCTGACCCCAAGTCACTATCTCTGAACTTATATTAATTGAGA 2138  
 Db 1921 GCGTGGGGAATCTCTGACCCCAAGTCACTATCTCTGAACTTATATTAATTGAGA 1980  
 Qy 2139 CCCATACCAAGACAAAGTACAGGAACTCAATATGACTCCCTCCCAAAAACTTA 2198  
 Db 1981 CCCATACCAAGACAAAGTACAGGAACTCAATATGACTCCCTCCCAAAAACTTA 2040  
 Qy 2199 TAAAAATGCAATGATGACACAAAGACAGCACTTTTGTACAGAGTGGGAGAGACTTT 2258  
 Db 2041 TAAAAATGCAATGATGACACAAAGACAGCACTTTTGTACAGAGTGGGAGAGACTTT 2100  
 Qy 2259 TTCTTGTATATGCTTATATTAATTAAGTCTATGGGCTGTTAAAAAAAACAGATTATTTAA 2318  
 Db 2101 TTCTTGTATATGCTTATATTAATTAAGTCTATGGGCTGTTAAAAAAAACAGATTATTTAA 2160  
 Qy 2319 AATTTAAAGCAAAAAAGTCAAAA 2341  
 Db 2161 AATTTAAAGCAAAAAAGTCAAAA 2183

RESULT 11  
 ABX80270

ID ABX80270 standard; DNA; 2185 BP.  
 AC ABX80270;  
 XX 28-APR-2003 (first entry)  
 DT XX  
 DE Novel human secreted or transmembrane protein PRO1344 DNA.  
 KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
 KW cardiac insufficiency disorder; cancer; tumour; immune response;  
 KW adrenal cortical capillary endothelial growth; c-fos induction;  
 KW vascular endothelial growth factor inhibition; VEGF inhibition;  
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
 KW retinal neurons cell survival; rod photoreceptor cell survival;  
 KW retinal disorder; retinitis pigmentosa; kidney disorder;  
 KW mammalian kidney mesangial cell proliferation; Berger disease;  
 KW dermatitis herpetiformis; Crohn's disease; chondrocyte proliferation;  
 KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US200232252-A1.  
 XX  
 PD 19-SEP-2002.  
 XX  
 PF 14-NOV-2001; 2001US-0990442.  
 XX  
 PR 05-NOV-1997; 97WO-US20069.  
 PR 16-SEP-1998; 98WO-US19330.  
 PR 17-SEP-1998; 98WO-US19437.  
 PR 07-OCT-1998; 98WO-US21141.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 05-JAN-1999; 99WO-US00106.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28301.  
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 PR 20-DEC-1999; 99WO-US30911.  
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 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
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 PR 11-JUN-1998; 98US-088861P.  
 PR 11-JUN-1998; 98US-088876P.  
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 PR 12-JUN-1998; 98US-089440P.  
 PR 16-JUN-1998; 98US-089512P.  
 PR 16-JUN-1998; 98US-089514P.  
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 PR 17-JUN-1998; 98US-089599P.  
 PR 17-JUN-1998; 98US-089600P.  
 PR 17-JUN-1998; 98US-089653P.  
 PR 18-JUN-1998; 98US-089801P.  
 PR 18-JUN-1998; 98US-089907P.  
 PR 18-JUN-1998; 98US-089908P.  
 PR 28-AUG-2001; 2001US-0941992.

(GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
 PI Berrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,  
 PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF,  
 PI Roy MA, Stewart TX, Tumas D, Watanabe CK, Williams PM, Wood WI,  
 PI Zhang Z;

WPI: 2003-247083/24.

DR P-PSDB; ABUS9111.

XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
 PT are therapeutically useful for enhancing immune response and in cancer  
 PT treatments

XX Claim 2, Fig 158; 6489P; English.

XX The invention describes an isolated human PRO polypeptide. The PRO  
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in  
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
 CC in modulating at least one biological activity of a cell expressing a PRO  
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO536  
 CC stimulate adrenal cortical capillary endothelial growth, and PRO536,

CC PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
 CC useful for treating conditions or disorders where angiogenesis would be  
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
 CC useful for treating cancerous tumours. PRO812 inhibits vascular  
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
 CC cells and is thus useful for inhibiting proliferation of endothelial  
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing  
 CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of  
 CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
 CC rod photoreceptor cells) and therefore are useful for treating retinal  
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
 CC and therefore are useful for treating kidney disorders associated with  
 CC decreased mesangial cell function such as Berger disease or other  
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's  
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
 CC proliferation and/or redifferentiation of chondrocytes in culture and  
 CC are thus useful for treating sports injuries, and arthritis. This  
 CC sequence represents a novel human PRO protein polynucleotide.

XX Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;

SQ Query Match 92.8%; Score 2171.8; DB 25; Length 2185;

Best Local Similarity 99.7%; Pred. No. 0; Mismatches 2176; Conservative 0; Indels 0; Gaps 0;

QY 159 GTTCTCTTCGAGCAAAATCCAGGCGATGGTGAATTATGAACTGCGACACATGA 218  
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 QY 219 AGCTTTGTGGCAGTACTGTGACACACACACTGGAATGCCATCTGCTCCGTTTCG 278  
 Db 61 AGCTTTGTGGCAGTACTGTGACACACACACTGGAATGCCATCTGCTCCGTTTCG 120  
 QY 279 TCTACCTCAGGCGGCAAGTGTGATTTGTGTGAGCATTCGCTGCGCCGCTCAACCG 338  
 Db 121 TCTACCTCAGGCGGCAAGTGTGATTTGTGTGAGCATTCGCTGCGCCGCTCAACCG 180  
 QY 339 GGCCCCAGAACTGCCCCCTCCGTCGTGCTGACAGTAACCAAGTTGAGAGGTGTGCA 398  
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 QY 399 CGCGCCGGGGCTCTCCGAGGTCCTCCGAGGGTATTCCTTGAACACCCGGTACTCAAC 458  
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 Db 301 TCAATGAGAACCAATCCATGATATCCAGGCCGACACCTCCGACACTCCACCACTGG 360  
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 DT 22-APR-2003 (first entry)  
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 KW diagnostic; biosensor; bioreactor; tumour; therapeutic;  
 KW gene therapy; tumour-associated antigenic target; TAT; ADSEPT;  
 KW antibody-dependent enzyme mediated prodnrg therapy; cytostatic.  
 OS Homo sapiens.  
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 PN US2003027162-A1.  
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Query Match 92.8%; Score 2171.8; DB 25; Length 2185;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2176; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 1659 GTTACAGCGGCAATATACCACTCTACCAAGGTGCTCATTCAGACTAACCCGTGCGCA 1718
DB 1501 GTTACAGCGGCAATATACCACTCTACCAAGGTGCTCATTCAGACTAACCCGTGCGCA 1560
QY 1719 AGCAGGTGGAGATACCCGCGCAAGACACACTGACAGAGTGCAGACAGCTGGATGAG 1778
DB 1561 AGCAGGTGGAGATACCCGCGCAAGACACACTGACAGAGTGCAGACAGCTGGATGAG 1620
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DB 1681 CCATGTTGATTTCTTATTAACCTTGTGAACGCGCAACAGACGGAATGACATCAAG 1740
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DB 1801 CAGCAACAGAGCTCGGTCCGGGTATCAGGTGAAGGGGCGAGTGTGTGCGCAATTC 1860
QY 2019 ATGACATATTAATTAACAACCTTACAAACAGGACATGTGGGCCCACTGACAGAAAAA 2078

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Query Match 92.8%; Score 2171.8; DB 25; Length 2185;  
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QY 219 AGCTCTGTGGCAGGTACTGTGTGCACACCAACACTGGAATGCCATCTGCTCCGGTTG 278  
DB 61 AGCTCTGTGGCAGGTACTGTGTGCACACCAACACTGGAATGCCATCTGCTCCGGTTG 120  
QY 279 TCTACTCAGCGCGCAAGTGTGATTTCTGTGTGCAGCCATGCTGTGCCGCTCAGCCG 338  
DB 121 TCTACTCAGCGCGCAAGTGTGATTTCTGTGTGCAGCCATGCTGTGCCGCTCAGCCG 180  
QY 339 GGGCCCAAGACTGCCCTCCGCTGCTGTGTGCAGTAACCACTTAGCAAGGTGTGTGA 398  
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DB 301 TCATGAGAAACAACATCCAGATGATCCAGCCCGACACCTTCCGCCACTCCACCACTGG 360  
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AC ABX90247;  
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DT 01-MAY-2003 (first entry)  
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DE Human secreted/transmembrane protein cDNA, #93.  
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KW Human; gene; ss; PRO; secreted; transmembrane; signal peptide;  
KW pharmaceutical; diagnostic; therapeutic; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PF 14-NOV-2001; 2001US-0992598.  
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XX 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
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PR 10-MAR-2000; 2000WO-US06319.  
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PR 01-DEC-2000; 2000WO-US32678.

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 PR 28-MAY-1998; 98US-087106P.  
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 PR 18-JUN-1998; 98US-089907P.  
 PR 18-JUN-1998; 98US-089908P.  
 PR 28-AUG-2001; 2001US-0941992.  
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 PA (GERTH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
 PI Ferrara N, Fong S, Geber H, Gerltsen ME, Goddard A, Godowski PJ,  
 PI Girmaldi JC, Gurney AJ, Kijavlin IJ, Napier MA, Pan J, Paoni NF,  
 PI Roy M, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WT,  
 PI Zhang Z;  
 XX  
 DR WPI; 2003-288106/28.  
 DR P-PSDB; ABU60541.  
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 PT New transmembrane polypeptides and nucleic acids encoding the  
 PT polypeptides, useful in gene therapy, in chromosome identification, as  
 PT chromosome markers, or in generating probes -  
 XX  
 PS Claim 2; Fig 156; 650pp; English.  
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CC The invention discloses isolated PRO secreted/transmembrane polypeptides  
 CC comprising a sequence without signal peptide and the nucleic acid  
 CC encoding them. The polypeptides can be used to raise antibodies that  
 CC specifically bind to the PRO polypeptide, for linking a bioactive  
 CC molecule to a cell expressing a PRO protein and for modulating at least  
 CC one biological activity of a cell. The PRO polypeptides or  
 CC polynucleotides are also useful in gene therapy, in chromosome  
 CC identification, as chromosome markers, or in generating probes. The PRO  
 CC electrophoresis, and the isolated nucleic acids may be used for  
 CC recombinantly expressing those markers. The PRO polypeptides and nucleic  
 CC acids may also be used in tissue typing. Anti-PRO antibodies are useful  
 CC in diagnostic assays for PRO, and in affinity purification of PRO from  
 CC recombinant cell culture or natural sources. The sequences presented in  
 CC ABX90083-ABX90468 are the genes encoding, the primers amplifying and the  
 CC probes detecting the PRO polynucleotides of the invention.  
 CC Note: The sequence data for this patent is also available in electronic  
 CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
 XX  
 SQ Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;

Query Match 92.8%; Score 2171.8; DB 25; Length 2185;  
 Best Local Similarity 99.7%; Pred. No. 0; Mismatches 7; Indels 0; Gaps 0;

Matches 2176; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY	279	TCTACCTCAGGGGCAAGTGTGATCTGTGTGAGCCATCGTGTGCGGCTCAGCCG	338
DB	121	TCTACCTCAGGGGCAAGTGTGATCTGTGTGAGCCATCGTGTGCGGCTCAGCCG	180
QY	339	GGCCCGGAGCTGCGCTCCGCTGTCTGTGAGTAACGATTGAGAGGTGTGTGCA	398
DB	181	GGCCCGGAGCTGCGCTCCGCTGTCTGTGAGTAACGATTGAGAGGTGTGTGCA	240
QY	399	CGCGCGGGGCTCTCCGAGGTCCGAGGGTATTCCTTGAAACCCGGTACTCAAC	458
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QY	459	TCAATGAGAACCAATCAATCAATGATTCAGGCGGACCTTCGACCTCCACCACTGG	518
DB	301	TCAATGAGAACCAATCAATCAATGATTCAGGCGGACCTTCGACCTCCACCACTGG	360
QY	519	AGGTCTGCAAGTGGGAGGAACTCCATCCGAGATTTGAGGTGGGGCTTCAACGGCC	578
DB	361	AGGTCTGCAAGTGGGAGGAACTCCATCCGAGATTTGAGGTGGGGCTTCAACGGCC	420
QY	579	TGGCAGCTTCAGACCTCGAGCTGTGACAACTGGCTGACAGTCATCTTACCGGGG	638
DB	421	TGGCAGCTTCAGACCTCGAGCTGTGACAACTGGCTGACAGTCATCTTACCGGGG	480
QY	639	CCTTGAATACCTGTCCAACTGGGGAGCTTGGCTTCCCAACCAACCCATGGAAGCA	698
DB	481	CCTTGAATACCTGTCCAACTGGGGAGCTTGGCTTCCCAACCAACCCATGGAAGCA	540
QY	699	TCCCTCTTACGCTTCAACCGGGTCCCTCCATGCGCCTGAGATTGGGGAGGCTCA	758
DB	541	TCCCTCTTACGCTTCAACCGGGTCCCTCCATGCGCCTGAGATTGGGGAGGCTCA	600
QY	759	AGAACTGAGATATATCTGAGGAGCTTTTGAAGGGCTGTTCACCTCAAGTATCTGA	818
DB	601	AGAACTGAGATATATCTGAGGAGCTTTTGAAGGGCTGTTCACCTCAAGTATCTGA	660
QY	819	ACTTGGGATGTGAAATTAAGACATGCCCAATTCACCCCTGTGGGGCTTGAAG	878
DB	661	ACTTGGGATGTGAAATTAAGACATGCCCAATTCACCCCTGTGGGGCTTGAAG	720

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Search completed: January 22, 2004, 16:23:06  
 Job time : 625 secs



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AP

RESULT 2  
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; Sequence 9, Application US/09957187  
; Publication No. US20030054514A1  
; GENERAL INFORMATION:  
; APPLICANT: Shimkels, Richard A.  
; APPLICANT: Larocheville, William  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY  
; FILE REFERENCE: 15966-540 CIP  
; CURRENT APPLICATION NUMBER: US/09/957,187  
; CURRENT FILING DATE: 2000-09-19  
; PRIOR APPLICATION NUMBER: 60/123,667  
; PRIOR FILING DATE: 1999-03-09  
; PRIOR APPLICATION NUMBER: 09/520,781  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: 60/234,082  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: 60/233,798  
; PRIOR FILING DATE: 2000-09-19  
; PRIOR APPLICATION NUMBER: 60/174,485  
; PRIOR FILING DATE: 2000-01-04  
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; NAME/KEY: CDS  
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US-09-957-187-9

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Best Local Similarity 100.0%; Pred. No. 0;  
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Db 121 AGAGAGACTCTCTACTCACTTAAGCCGGGGTAAAGGCTGTCTCTTTCCAGACCAAAAT 180  
Qy 181 CCCAGGAGATGTAATTAATTAAGAGTGGACACACCATGAGTCTTGTGGCAGTAACTGT 240  
Db 181 CCCAGGAGATGTAATTAATTAAGAGTGGACACACCATGAGTCTTGTGGCAGTAACTGT 240  
Qy 241 GCACACACCAACCTGGAATGCGATCTGCTCCGTTGCTTCACTCAAGGCGCAAGTGTG 300  
Db 241 GCACACACCAACCTGGAATGCGATCTGCTCCGTTGCTTCACTCAAGGCGCAAGTGTG 300  
Qy 301 GATTCTGTGGACCACTGCTGCTGCTGCGCTCAAGCCGGGCCCAAGAACTCCCTCCGT 360  
Db 301 GATTCTGTGGACCACTGCTGCTGCTGCGCTCAAGCCGGGCCCAAGAACTCCCTCCGT 360  
Qy 361 CTGCTCTGTGAGTAACTGATCAGCAAGTGTGTGACGCGCGGGGCTCTCCGAGGT 420  
Db 361 CTGCTCTGTGAGTAACTGATCAGCAAGTGTGTGACGCGCGGGGCTCTCCGAGGT 420  
Qy 421 CCGCAGGAGTATTCCTCTGAAACACCCGGTACCTCAACTGAGAAACAATCCAGAT 480  
Db 421 CCGCAGGAGTATTCCTCTGAAACACCCGGTACCTCAACTGAGAAACAATCCAGAT 480

Db 421 CCGCAGGAGTATTCCTCTGAAACACCCGGTACCTCAACTGAGAAACAATCCAGAT 480  
Qy 481 GATCCAGGCGGACACCTTCCGCCACCTCCACACCTGAGAGTCTTGAGTGGGACAGAA 540  
Db 481 GATCCAGGCGGACACCTTCCGCCACCTCCACACCTGAGAGTCTTGAGTGGGACAGAA 540  
Qy 541 CTCATCCGAGCAATTAAGTGGGGGCTTCAACCGGCTGGCCAGCCTCAGACCTTGA 600  
Db 541 CTCATCCGAGCAATTAAGTGGGGGCTTCAACCGGCTGGCCAGCCTCAGACCTTGA 600  
Qy 601 GCTGTGAGCAACTGAGTGAAGTCACTCCCTAGCGGGGCTTTGAATCTGTCCAGGT 660  
Db 601 GCTGTGAGCAACTGAGTGAAGTCACTCCCTAGCGGGGCTTTGAATCTGTCCAGGT 660  
Qy 661 GCGGAGCTCTGGCTTGGCAACAACCCCATCGAAGAGTCCCTTAGCGCTTCAACCG 720  
Db 661 GCGGAGCTCTGGCTTGGCAACAACCCCATCGAAGAGTCCCTTAGCGCTTCAACCG 720  
Qy 721 GGTGCTCTCCCTCATGCGCTGAGCTTGGGGAGCTTCAGAGCTGAGTATCTCTGA 780  
Db 721 GGTGCTCTCCCTCATGCGCTGAGCTTGGGGAGCTTCAGAGCTGAGTATCTCTGA 780  
Qy 781 GGGAGCTTTGAGGGGCTGTTCAACCTCAAGTATCTGAATCTGGGCAATGCAATTAA 840  
Db 781 GGGAGCTTTGAGGGGCTGTTCAACCTCAAGTATCTGAATCTGGGCAATGCAATTAA 840  
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Db 841 AGACATGCCAATCTCAACCCCGTGGGGGCTGAGAGAGCTGGAGATGTCAGGGAACA 900  
Qy 901 CTTCCCTGAGATCAGGCTGCTCTTTCATAGGCTGAGCTCCCTCAAGAGCTCTGGGT 960  
Db 901 CTTCCCTGAGATCAGGCTGCTCTTTCATAGGCTGAGCTCCCTCAAGAGCTCTGGGT 960  
Qy 961 CATGAATCTCAGAGTCAAGCTGATGAGCGGAATGCTTTTGAACGGGCTTCACTTGT 1020  
Db 961 CATGAATCTCAGAGTCAAGCTGATGAGCGGAATGCTTTTGAACGGGCTTCACTTGT 1020  
Qy 1021 GGAATCAACTGGGCGGACAAATACCTCTCTTTGGCCCATGAGCTCTTTTACCGGCT 1080  
Db 1021 GGAATCAACTGGGCGGACAAATACCTCTCTTTGGCCCATGAGCTCTTTTACCGGCT 1080  
Qy 1081 GAGGTACCTGATGAGTGTGATCTACACCAACCTTGGAACTGTGATGTGACATTTCT 1140  
Db 1081 GAGGTACCTGATGAGTGTGATCTACACCAACCTTGGAACTGTGATGTGACATTTCT 1140  
Qy 1141 GTGGCTAGCTGTGGCTGTTGAGAGTAAATCCCAATTCACCTGTGTGGCGCTG 1200  
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Qy 1201 TCATGCTCCCATGACATGAGAGCGGCTACCTGTGAGAGTGAACAGAGCTCTCTTCA 1260  
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Qy 1261 GTGCTGCCCCCTTCACTATGAGACGACCTCGAACCTCAACATTTCTGAGGGTCCGAT 1320  
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Qy 1321 GGCAGAACTTAAGTGGGAATCCCTATGTCTCCGTGAAGTGTGTGCTGCCAATGG 1380  
Db 1321 GGCAGAACTTAAGTGGGAATCCCTATGTCTCCGTGAAGTGTGTGCTGCCAATGG 1380  
Qy 1381 GACAGTCTCAGACACCTCTCCGACCAACCAAGATCTGTCTTCAACAGACGACCTT 1440  
Db 1381 GACAGTCTCAGACACCTCTCCGACCAACCAAGATCTGTCTTCAACAGACGACCTT 1440  
Qy 1441 GAACTTTTCCACAGTGTCTTTCAGACATGGGGTGAACAATGAGGAGCAATGT 1500  
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Qy 1501 TGACGCAACTCCAAAGCTCTGAGCTTCAATGAGAGCAAGGCTGAGCTTAAACCTTC 1560  
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[illegible]

Db	841	AGACATGCCCAATCTCAACCCCTGTGTGGGGCTTGGAGAGCTGGAGATGTCAAGGAACCA	900
OY	901	CTTCCCTGAGATCAAGGCGCTGGCTCTTTCATATGGCCCTGAGCTCCCTCAAGAAAGCTCTGGGT	960
Db	901	CTTCCCTGAGATCAAGGCGCTGGCTCTTTCATATGGCCCTGAGCTCCCTCAAGAAAGCTCTGGGT	960
OY	961	CATBAATCAAGGTCACGCTGATTTAGAGCGGAATGCTTTTAAAGGGCTGGCTTCACTTGT	1020
Db	961	CATBAATCAAGGTCACGCTGATTTAGAGCGGAATGCTTTTAAAGGGCTGGCTTCACTTGT	1020
OY	1021	GGAATCAAACTTGGCGCCCAATTAACCTCTCTTCTTGGCCCATGACCTCTTAAACCCGCT	1080
Db	1021	GGAATCAAACTTGGCGCCCAATTAACCTCTCTTCTTGGCCCATGACCTCTTAAACCCGCT	1080
OY	1081	GAGGTACCTGTGTGAGTGGATCTTACACACACACCTTTGAACTGTGATTTGTGACATTTCT	1140
Db	1081	GAGGTACCTGTGTGAGTGGATCTTACACACACACCTTTGAACTGTGATTTGTGACATTTCT	1140
OY	1141	GTGGCTAGCCCTGTGTGGCTTTCGAGAGTAAATACCCAAATTCACCTGTCTGTGGCCGCTG	1200
Db	1141	GTGGCTAGCCCTGTGTGGCTTTCGAGAGTAAATACCCAAATTCACCTGTCTGTGGCCGCTG	1200
OY	1201	TCATGCTCCCATGACACATGCGAGGCGGTACCTCGTGGAGGTGGACAGGCGCTCCTTCCA	1260
Db	1201	TCATGCTCCCATGACACATGCGAGGCGGTACCTCGTGGAGGTGGACAGGCGCTCCTTCCA	1260
OY	1261	GTGCTCTGGCCCCCTTCATCATGAGACGCACTCGAGACCTCAAACTTCTGAGGGTCCGAT	1320
Db	1261	GTGCTCTGGCCCCCTTCATCATGAGACGCACTCGAGACCTCAAACTTCTGAGGGTCCGAT	1320
OY	1321	GGCAGAACTTAAATGTGCGAATCCCCCTTAATGTCTCTCGTGAATGTGTGCTGCCAATGG	1380
Db	1321	GGCAGAACTTAAATGTGCGAATCCCCCTTAATGTCTCTCGTGAATGTGTGCTGCCAATGG	1380
OY	1381	GACAGTGTCAAGCAACGCGCTCCCGCACCCCAAGAGATCTCTGCTCCCAACGACGCACTT	1440
Db	1381	GACAGTGTCAAGCAACGCGCTCCCGCACCCCAAGAGATCTCTGCTCCCAACGACGCACTT	1440
OY	1441	GAACTTTTCCCAACGCTGTCTTTTCAAGCACTGGGGTGTACATGCAATGGGGAAACCAATGT	1500
Db	1441	GAACTTTTCCCAACGCTGTCTTTTCAAGCACTGGGGTGTACATGCAATGGGGAAACCAATGT	1500
OY	1501	TGCAGGCAATCCAAACGCTGTGGCTTCACTGATGGAGCAACGCGTGAAGCTTAAACCTTC	1560
Db	1501	TGCAGGCAATCCAAACGCTGTGGCTTCACTGATGGAGCAACGCGTGAAGCTTAAACCTTC	1560
OY	1561	CAACTCAACGCTTCTTCAACACAGAGAAAGGGGAGACCAAGAGATCTGCGCTGAGAGACAC	1620
Db	1561	CAACTCAACGCTTCTTCAACACAGAGAAAGGGGAGACCAAGAGATCTGCGCTGAGAGACAC	1620
OY	1621	AACGGGAAGTACAAAGCCTGTTTCCCTACACAGCTCCACTGTATTACAGCCGGCATATACAC	1680
Db	1621	AACGGGAAGTACAAAGCCTGTTTCCCTACACAGCTCCACTGTATTACAGCCGGCATATACAC	1680
OY	1681	CTCTACCAACGCTGTCTCATTTAGACTAACCCGCTGTGCCAAGCAGGCTGGCAGTACCGCGAC	1740
Db	1681	CTCTACCAACGCTGTCTCATTTAGACTAACCCGCTGTGCCAAGCAGGCTGGCAGTACCGCGAC	1740
OY	1741	AGACACCACTACAAAGATGACAGACCAAGCCTGGATGAATCATGGAAGACCAACCAAGATAT	1800
Db	1741	AGACACCACTACAAAGATGACAGACCAAGCCTGGATGAATCATGGAAGACCAACCAAGATAT	1800
OY	1801	CATTGGCTGCTTTTGTGGCAGTGACTCTGTAGCTGCGCCCATGTTGATTTGCTTCTATPAA	1860
Db	1801	CATTGGCTGCTTTTGTGGCAGTGACTCTGTAGCTGCGCCCATGTTGATTTGCTTCTATPAA	1860
OY	1861	ACTTGTAAGCGGCAACAGACGCGAGTACAGTCAACACCGCGCCCACTGTGAGAGAAA	1920
Db	1861	ACTTGTAAGCGGCAACAGACGCGAGTACAGTCAACACCGCGCCCACTGTGAGAGAAA	1920
OY	1919	ATCCAGGTGACGAAGACATCCCAAGACCAATCCGACAGCAACAGCAAGCTCTCGTCC	1978
Db	1921	ACACAGGACAAAAACAACAACAACAACAACAACAACAACAACAACAAGCCCCCCCC	1980

QY	1979	GGTGTATACAGGTGAAGGGGGAGTGTGTGTGTCGCCCAATTTATGACCATATTTAATAAGAC	2038
Db	1981	GGTATTAACAGGAAGGGGACATATGTCCGCCCAAAAACAACAACATTAATAAAACAAAC	2040
QY	2039	ACCTTAACAAACAGACACATGGGGGCCACTGACACAGAAAACAGCCTGTGGGAACTCTCTGCAC	2098
Db	2041	ACACACAAACAGACACATGGGGGCCCACTGGACACAAAAACAGCCTGTGGGAACTCTGTGCAC	2100
QY	2099	CCCAAGTACACCATATCTCTGAACTTTATTAATTAGACCCATACCAAGACAAAGTA	2158
Db	2101	CCCAAGTACACCATATCTCTGAACTTTATTAATTAGACCCCAATACCAAGACAAAGTA	2160
QY	2159	CAGAAAACTAATATGATCTCCCTCCGCCCAAAAACCTTTAAATGCAATAGAAATGCAC	2218
Db	2161	CAGAAAACTAATATGATCTCCCTCCGCCCAAAAACCTTTAAATGCAATAGAAATGCAC	2220
QY	2219	ACAAAGACAGCACTTTTGTACAGAGTGGGAGAGACTTTTCTTGATATGCTTAATATA	2278
Db	2221	ACAAAGACAGCACTTTTGTACAGAGTGGGAGAGACTTTTCTTGATATGCTTAATATA	2280
QY	2279	TTAAGTCTATGGGCTGGTTAAAAAACAGATTATTTAAATTTAAAGACAAAAAGTCA	2338
Db	2281	TTAAGTCTATGGGCTGGTTAAAAAACAGATTATTTAAATTTAAAGACAAAAAGTCA	2340
QY	2339	AAA 2341	
Db	2341	AAA 2343	
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US-09-957-187-11			
; Sequence 11, Application US/09957187			
; Publication No. US20030054514A1			
; GENERAL INFORMATION:			
; APPLICANT: Shinketsu, Richard A.			
; APPLICANT: Labocheille, William			
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY			
; FILE REFERENCE: 15965-540 CIP			
; CURRENT APPLICATION NUMBER: US/09/957,187			
; CURRENT FILING DATE: 2000-09-19			
; PRIOR APPLICATION NUMBER: 60/123,667			
; PRIOR FILING DATE: 1999-03-09			
; PRIOR APPLICATION NUMBER: 09/520,781			
; PRIOR FILING DATE: 2000-03-03			
; PRIOR APPLICATION NUMBER: 60/234,082			
; PRIOR FILING DATE: 2000-09-20			
; PRIOR APPLICATION NUMBER: 60/233,798			
; PRIOR FILING DATE: 2000-09-19			
; PRIOR APPLICATION NUMBER: 60/174,485			
; PRIOR FILING DATE: 2000-01-04			
; NUMBER OF SEQ ID NOS: 85			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 11			
; LENGTH: 2607			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (215) .. (1984)			
US-09-957-187-11			
Query/ Match			
Best Local Similarity 95.9%; Score 2244.2; DB 11; Length 2607;			
Matches 2288; Conservative 0; Mismatches 53; Indels 2; Gaps 1;			
QY	1	CACCTTCCCTTTTGTATTAATTAACCTAAGAGTCGAAATGGGAACGAGTGCCAGCTC	60
Db	1	CACCTTCCCTTTTGTATTAATTAACCTAAGAGTCGAAATGGGAACGAGTGCCAGCTC	60
QY	61	CCGTGGAGAAAGCTTAAGAGACACAGCGCAGTGCTTTCTGTGCTTCTTCCGAGATGAA	120
Db	61	CCGTGGAGAAAGCTTAAGAGACACAGCGCAGTGCTTTCTGTGCTTCTTCCGAGATGAA	120

QY 121 AGAGAGCTCTAGCTCACTTAAGCCGGGCTAGGGCTGTTCTCTTTCCGAGCCAAAT 180  
 DB 121 AGAGAGCTCTAGCTCACTTAAGCCGGGCTAGGGCTGTTCTCTTTCCGAGCCAAAT 180  
 QY 181 CCCAGGCGATGTGTAATTATGAAAGTGCACACCATGAAGCTCTTGTGGCAGTAACTGT 240  
 DB 181 CCCAGGCGATGTGTAATTATGAAAGTGCACACCATGAAGCTCTTGTGGCAGTAACTGT 240  
 QY 241 GCACACCAACACCTGGAATGTCATCTGCTCCGCTGCTACCTCAACGCGGCAAGTGTG 300  
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 QY 301 GATTCTGTGTGACAGCATCTGCTGCTGACCCGCTCAAGCCGAGCAATCTGCTCCGT 360  
 DB 301 GATTCTGTGTGACAGCATCTGCTGCTGACCCGCTCAAGCCGAGCAATCTGCTCCGT 360  
 QY 361 CTGCTCTGTGAGTAACCATTTCAAGCAAGTGTGTGACGCGCGGGGCTCTCCAGGT 420  
 DB 361 CTGCTCTGTGAGTAACCATTTCAAGCAAGTGTGTGACGCGCGGGGCTCTCCAGGT 420  
 QY 421 CCCGCAAGGCTATTCCTCTGGAACACCCGCTACCTCACTCATGGAACCAATCCAGAT 480  
 DB 421 CCCGCAAGGCTATTCCTCTGGAACACCCGCTACCTCACTCATGGAACCAATCCAGAT 480  
 QY 481 GATCCAGGCGGACACTTCCGCACTTCACACCATGAGGCTCTGCACTTGGCAGGAA 540  
 DB 481 GATCCAGGCGGACACTTCCGCACTTCACACCATGAGGCTCTGCACTTGGCAGGAA 540  
 QY 541 CTCCATCCGCGCAATTAAGTGTGGGGGCTTCAACGCGCTGCGCACAGCTCAGCACTGGA 600  
 DB 541 CTCCATCCGCGCAATTAAGTGTGGGGGCTTCAACGCGCTGCGCACAGCTCAGCACTGGA 600  
 QY 601 GCTGTGCAACAATGAGTGTGAGTGTGGGGGCTTGAATTCCTGTCAGAGCT 660  
 DB 601 GCTGTGCAACAATGAGTGTGAGTGTGGGGGCTTGAATTCCTGTCAGAGCT 660  
 QY 661 GCGGAGAGCTCTGAGCTGCGCAACAACCCCATGAAAGCTCCCTCTTACGCTTCAACCG 720  
 DB 661 GCGGAGAGCTCTGAGCTGCGCAACAACCCCATGAAAGCTCCCTCTTACGCTTCAACCG 720  
 QY 721 GGTGCTCTCTCATGCGCTGGAACCTTGGGGAGCTCAAGAGCTGAGTATATCTGGA 780  
 DB 721 GGTGCTCTCTCATGCGCTGGAACCTTGGGGAGCTCAAGAGCTGAGTATATCTGGA 780  
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 DB 781 GGGAGCTTTTGAAGGGGCTGTTCACATTCATTCGAACTTGGGCAATGTCACATTTAA 840  
 QY 841 AGACATGCGCAATCTCAACCCCTCTGTGTGGGCTGAGAGCTGAGATGTAGGGAACA 900  
 DB 841 AGACATGCGCAATCTCAACCCCTCTGTGTGGGCTGAGAGCTGAGATGTAGGGAACA 900  
 QY 901 CTTCCTGTGAGTCAAGGCTGTGCTCTTTCATGAGCTGAGCTCCCTCAAGAGCTGTGGT 960  
 DB 901 CTTCCTGTGAGTCAAGGCTGTGCTCTTTCATGAGCTGAGCTCCCTCAAGAGCTGTGGT 960  
 QY 961 CATGAATCTCAAGTCAAGCTGATTTGAGCGGAATGCTTTTGAAGGGGCTGTCACTTGT 1020  
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 DB 1021 GGAATCTCAACTTGGCCCAATTAACCTCTCTTTTGGCCCATGACCTCTTTTACCCGCT 1080  
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 DB 1081 GAGGTACTGTGTGAGTGTGATCTACACCAACACCTTGAATCTGTGAATTTGACATTTCT 1140  
 QY 1141 GTGGCTAGCTGTGTGAGTGTGAGATTAATACCAACCAATTCACCTGCTGTGGCGCTG 1200  
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QY 1201 TCATGCTCCCATGACATGCGAGGCGCTACCTGTGTGAGGTGAGCCAGGCTCTTCCA 1260  
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 QY 1261 GTGCTTGGCCCCCTTATTCATGAGACGACCTCCAGACTTCAACATTTCTGAAGGTCCGAT 1320  
 DB 1261 GTGCTTGGCCCCCTTATTCATGAGACGACCTCCAGACTTCAACATTTCTGAAGGTCCGAT 1320  
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 DB 1441 GAACTTTTCCACGCTGTGCTTTTCAAGCACTGGGGGTATACATGATGGGAGCAATGT 1500  
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 DB 1561 CAATCAAGCTTCTTCAACAAGAACAGGGAGAACCAAGAGATCTCGCTGAGACAC 1620  
 QY 1621 AACGCGAAATGTAAGAGCTGTCTTCTTCAAGCTGATTCAGAGCTGATTAATACAC 1680  
 DB 1621 AACGCGAAATGTAAGAGCTGTCTTCTTCAAGCTGATTCAGAGCTGATTAATACAC 1680  
 QY 1681 CTCTACCAAGGCTGCTCAATTAAGACTACCCGCTGAGGAGGAGTGCAGTACCCGAGAC 1740  
 DB 1681 CTCTACCAAGGCTGCTCAATTAAGACTACCCGCTGAGGAGGAGTGCAGTACCCGAGAC 1740  
 QY 1741 AGACACCACTGACAAAGATGACACACAGCTGTGATGAAGTATGAAAGCAACCAAGATCAT 1800  
 DB 1741 AGACACCACTGACAAAGATGACACACAGCTGTGATGAAGTATGAAAGCAACCAAGATCAT 1800  
 QY 1801 CATTGGCTGCTTGTGTGCACTGACTGTCTGATGCTGCGGCAATGTGATTTGCTTATTA 1860  
 DB 1801 CATTGGCTGCTTGTGTGCACTGACTGTCTGATGCTGCGGCAATGTGATTTGCTTATTA 1860  
 QY 1861 ACTTCGTAAAGGGGACAGGAGCGAGTACAGTCAAGACCGG--CCGGAAGCTTGAAGATA 1920  
 DB 1861 ACTTCGTAAAGGGGACAGGAGCGAGTACAGTCAAGACCGG--CCGGAAGCTTGAAGATA 1920  
 QY 1921 ACACAGGAGCAAAAACACACACAAACAAACCCCAACAAACAAACAGCCCCCCC 1980  
 DB 1921 ACACAGGAGCAAAAACACACACAAACAAACCCCAACAAACAAACAGCCCCCCC 1980  
 QY 1981 GGTGTATCAGGTGAAGGGGAGTATGTGCTGCCAATTCATGACCTATTAATTAACAC 2040  
 DB 1981 GGTGTATCAGGTGAAGGGGAGTATGTGCTGCCAATTCATGACCTATTAATTAACAC 2040  
 QY 2041 ACCTAAGCAACAGCAATGAGGAGCCCACTGGAAGAAACAGCTGGGAACTCTCTGAC 2100  
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 QY 2101 CCCAGAGTCAACATATCTGAACTTATTAATTAATTAATTAATTAATTAATTAATTAATTA 2160  
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 QY 2221 ACAAGGACACCACTTTTGTACAGAGTGGGAGAGACTTTTCTTGTATATGCTTATTAATA 2280  
 DB 2221 ACAAGGACACCACTTTTGTACAGAGTGGGAGAGACTTTTCTTGTATATGCTTATTAATA 2280  
 QY 2279 TTAAGTCTATGGGCTGTAAAAAAACAGATTATTAATTAATTAATTAATTAATTAATTA 2338



Db 2281 TTAAGTCTAAGGCTGGTTAAAAAACAATTATTAATTAAGCAAAAAAGCTCA 2340  
 Qy 2339 AAA 2341  
 Db 2341 AAA 2343

RESULT 5

US-09-989-722-228  
 ; Sequence 228, Application US/09989722  
 ; Patent No. US20020072067A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
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 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerltzen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Grimaldi, Paul J.  
 APPLICANT: Gunney, Austin L.  
 APPLICANT: Kijavini, Ivar J.  
 APPLICANT: Nadler, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730P1G3

CURRENT FILING DATE: 2001-11-19  
 CURRENT APPLICATION NUMBER: US/09/989,722

PRIOR FILING DATE: 1997-06-16  
 PRIOR APPLICATION NUMBER: 60/049787  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-11-12  
 PRIOR APPLICATION NUMBER: 60/065186  
 PRIOR FILING DATE: 1997-11-13  
 PRIOR APPLICATION NUMBER: 60/065311  
 PRIOR FILING DATE: 1997-11-24  
 PRIOR APPLICATION NUMBER: 60/066770  
 PRIOR FILING DATE: 1997-11-24  
 PRIOR APPLICATION NUMBER: 60/075945  
 PRIOR FILING DATE: 1998-02-25  
 PRIOR APPLICATION NUMBER: 60/078910  
 PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: 60/083322  
 PRIOR FILING DATE: 1998-04-28  
 PRIOR APPLICATION NUMBER: 60/084600  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/087106  
 PRIOR FILING DATE: 1998-05-28  
 PRIOR APPLICATION NUMBER: 60/087607  
 PRIOR FILING DATE: 1998-06-02  
 PRIOR APPLICATION NUMBER: 60/087609  
 PRIOR FILING DATE: 1998-06-02  
 PRIOR APPLICATION NUMBER: 60/087759  
 PRIOR FILING DATE: 1998-06-02  
 PRIOR APPLICATION NUMBER: 60/087827  
 PRIOR FILING DATE: 1998-06-03  
 PRIOR APPLICATION NUMBER: 60/088021  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088025

PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088026  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088028  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088029  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088030  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088033  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088326  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088167  
 PRIOR FILING DATE: 1998-06-05  
 PRIOR APPLICATION NUMBER: 60/088202  
 PRIOR FILING DATE: 1998-06-05  
 PRIOR APPLICATION NUMBER: 60/088212  
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 PRIOR APPLICATION NUMBER: 60/088217  
 PRIOR FILING DATE: 1998-06-05  
 PRIOR APPLICATION NUMBER: 60/088655  
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 PRIOR APPLICATION NUMBER: 60/088738  
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 PRIOR APPLICATION NUMBER: 60/088861  
 PRIOR FILING DATE: 1998-06-11  
 PRIOR APPLICATION NUMBER: 60/088876  
 PRIOR FILING DATE: 1998-06-11  
 PRIOR APPLICATION NUMBER: 60/089105  
 PRIOR FILING DATE: 1998-06-12  
 PRIOR APPLICATION NUMBER: 60/089440  
 PRIOR FILING DATE: 1998-06-16  
 PRIOR APPLICATION NUMBER: 60/089512  
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Query Match 92.8%; Score 2171.8; DB 9; Length 2185;  
Best Local Similarity 99.7%; Pred. No. 0;  
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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Geriltsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumaas, Daniel  
; APPLICANT: Tumaas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PLC62  
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; CURRENT FILING DATE: 2001-11-19  
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Query Match 92.8%; Score 2171.8; DB 9; Length 2185;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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 Db 1201 TGAAGTGTGTGCTGCGCAATGAGGACAGTGTCAAGCAAGCTCCCGGCAACCAAGATCT 1260  
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 Db 1561 AGCAGGTGGAGTACCCGCGAGACAGACCACTGACAAAGTGCAGACAGCTGAGTGAAG 1620  
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RESULT 7  
 US-09-969-279-228  
 Sequence 228, Application US/09989279  
 Patent No. US20020072496A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C56  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
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 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Query Match 92.8%; Score 2171.8; DB 9; Length 2185;  
 Best Local Similarity 99.7%; Pred. No. 0;  
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 DB 61 AGCTCTGTGGCAGTAAGTGTGACCAACACCTGGAATGCATCTGCTCCGTTG 120  
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 QY 339 GGGCCCAAGAACTGCGCCCTCCTGCTGCTGCTGCAAGTGAACCAAGTGTGCA 398  
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 QY 399 CGCGCCGGGGCTCTCCGAGGTCCGCGAGGTATTCCTCGAACAACCGGTAACCTCAAC 458  
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 QY 2319 AATTTAAGACAAAAGTCAAAA 2341  
 DB 2161 AATTTAAGACAAAAGTCAAAA 2183

RESULT 8  
 US-09-989-727-228  
 Sequence 228, Application US/09989727

Patent No. US20020072497A1  
 GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
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 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730PLC65  
 CURRENT FILING DATE: 2001-11-19  
 PRIOR APPLICATION NUMBER: US/09/989,727  
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PRIOR FILING DATE: 1998-07-09

Query Match 92.8%; Score 2171.8; DB 9; Length 2185;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2176; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerltzen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Kijavini, Ivar J.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC70  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR FILING DATE: 1997-10-17  
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 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

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 1501 GTTACAGCGGCGCATATACCACTTCAAGAGTGTCTCAATTCAGACTACCGGTGCGCA 1560  
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 1561 AGCAGGTGCAATACCCGCGACAGACCACTGACAAAGTGAAGCAAGCTGTGATGAAG 1620  
 1779 TCATGAAGACCAACCAATATCATATGCTGCTTTGGGAGAGTCACTGTAGCTGCGG 1838  
 1621 TCATGAAGACCAACCAATATCATATGCTGCTTTGGGAGAGTCACTGTAGCTGCGG 1680  
 1839 CATGTGATTTGTTCTATTAACCTTGTGAAGCGGCACAGCAAGGAGTCAAGTCAAG 1898



PRIOR APPLICATION NUMBER: 60/089512  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
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PRIOR FILING DATE: 1998-06-17  
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PRIOR FILING DATE: 1998-06-23  
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PRIOR APPLICATION NUMBER: 60/090862  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863

PRIOR FILING DATE: 1998-06-26  
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PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
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PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 92.8%; Score 2171.8; DB 10; Length 2185;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2176; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY GTTCTCTTCCGAGCCAAATCCAGCGCATGTGAATTATGAACGTGCCACACATGA 218  
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Db TCTACTCAGCGGCGCAAGTGTGATTTCTGTGTGAGCCATCGCTGCGGCTCAGCCG 180  
QY 339 GGCCCAGAACTGCCCTCCGTCTGTCTGTGAGTAACCAATTACAGAGTGTGTGA 398  
Db 181 GGCCCAGAACTGCCCTCCGTCTGTCTGTGAGTAACCAATTACAGAGTGTGTGA 240  
QY CGCGCCGGGGCTCTCCGAGGTCCCGAGGGTATTCCTCGAACCCTGTAACCTCAAC 458  
Db 241 CGCGCCGGGGCTCTCCGAGGTCCCGAGGGTATTCCTCGAACCCTGTAACCTCAAC 300  
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Db 301 TCATGAGAAACAATCATCATGATTCAGGCCGACCTTCCGACCTCCACCACTGG 360  
QY AGTCTCTGAGTGGGAGGAACTCATCCGAGATTGAGTGGGGCTTCAACGGCC 578  
Db 361 AGTCTCTGAGTGGGAGGAACTCATCCGAGATTGAGTGGGGCTTCAACGGCC 420  
QY TGGCAGCTTCAGCACTCTGAGCTGTTCAACAATGGCTGACAGTATCTCTACGCGGG 638  
Db 421 TGGCAGCTTCAGCACTCTGAGCTGTTCAACAATGGCTGACAGTATCTCTACGCGGG 480  
QY CCTTGAATCTCTGCAAGCTGGGAGCTTGGCTTCCGAACAACCCATGGAAGCA 698  
Db 481 CCTTGAATCTCTGCAAGCTGGGAGCTTGGCTTCCGAACAACCCATGGAAGCA 540  
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Db 601 AGAAGCTGAGTATATCTGAGGAGCTTTTGAAGGGCTGTTCAACCTCAAGTATCTGA 660  
QY ACTGGGCAATGTGAACATTAAGACATGCCCAATTCACCCCTGTGGGGCTGAGG 878  
Db 661 ACTGGGCAATGTGAACATTAAGACATGCCCAATTCACCCCTGTGGGGCTGAGG 720  
QY AGTGAAGATGTGAGGAAACCACTTCCCTGAGATCAGGCTGTGCTCTTCATGAGCTGA 938

Db 721 AGCTGAGATGTCAGGAGACCACTCCCTGAGATCAGAGCCCTGCTCTTCATGAGCCCTGA 780  
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 Qy 999 TTGACGGGCTGCTTCACTTGTGGAATCAACTTGGCCCAATATACCTCTCTTCTTGGC 1058  
 Db 841 TTGACGGGCTGCTTCACTTGTGGAATCAACTTGGCCCAATATACCTCTCTTCTTGGC 900  
 Qy 1059 CCCATGACCTTTTAACTCCCGCTGAGTACTGTGTGAGTTGATCTTACCAACACCTTT 1118  
 Db 901 CCCATGACCTTTTAACTCCCGCTGAGTACTGTGTGAGTTGATCTTACCAACACCTTT 960  
 Qy 1119 GGAACGTGATTTGATGATCTGTGGGCTAGCTGTGGCTTGGAGATATATATACCAACCA 1178  
 Db 961 GGAACGTGATTTGATGATCTGTGGGCTAGCTGTGGCTTGGAGATATATATACCAACCA 1020  
 Qy 1179 ATTCCACCTGCTGTGGGCTGTGATGCTCCCATGCAATGCGAGCCGCTACCTCGTGG 1238  
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 Db 1141 TCAACATTTTCTGAGGAGGTGGAATGGCAAACTTAATGTGCGAGCTCCCTATATGCTCCG 1200  
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 Db 1321 ACAATGATGAGGAGGACCAATGTTGCAAGCACTCAACGCTCGGCTTAACTCAATGGGA 1380  
 Qy 1539 GCACGGCTGAGCTTAACTCCCACTCAAGCTTCTTCAACCAAGAGGAGGAGCA 1598  
 Db 1381 GCACGGCTGAGCTTAACTCCCACTCAAGCTTCTTCAACCAAGAGGAGGAGCA 1440  
 Qy 1599 CGAGATCTGCTGAGGACCAACGCGAAAGTAAAGCCCTGTTCTTCAACCACTGCACTG 1658  
 Db 1441 CGAGATCTGCTGAGGACCAACGCGAAAGTAAAGCCCTGTTCTTCAACCACTGCACTG 1500  
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 Db 1501 GTTACACGCGGAGTATACCACTCTTCAACGAGGCTTCACTTCAACCACTGCTGCGCA 1560  
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 Db 1561 AGCAGGTGAGTACCGCGAGACACCACTGACAGATGCAAGATGCAAGCCTGATGATGA 1620  
 Qy 1779 TCATGAAGACCAAGATCACTTGTGCTTGTGAGAGTACTGTGCTGCTGCGC 1838  
 Db 1621 TCATGAAGACCAAGATCACTTGTGCTTGTGAGAGTACTGTGCTGCTGCGC 1680  
 Qy 1839 CCATGTTGATGTTCTTCTATTAATCTGTGAAGCGGACACAGACGAGTACATGACAG 1898  
 Db 1681 CCATGTTGATGTTCTTCTATTAATCTGTGAAGCGGACACAGACGAGTACATGACAG 1740  
 Qy 1899 CCGCCCGGAGCTGTGAGATATCCAGGTGAGAGAGATCCAGACAGCAATCCGAG 1958  
 Db 1741 CCGCCCGGAGCTGTGAGATATCCAGGTGAGAGAGATCCAGACAGCAATCCGAG 1800  
 Qy 1959 CAGCAACAGAGCTCCGCTCGGTATCAAGGTGAAGGGGAGTGTGCTGCCAATTC 2018

Db 1801 CAGCAACAGAGCTCCGCTCGGTATCAAGTGAAGGGGAGTGTGCTGCCAATTC 1860  
 Qy 2019 ATGACCATATTATTAATCAACACCTTACAAACACAGACATGGAGGCCCATGAGACAGAAACA 2078  
 Db 1861 ATGACCATATTATTAATCAACACCTTACAAACACAGACATGGAGGCCCATGAGACAGAAACA 1920  
 Qy 2079 GCCTGGGGAATCTCTGACACCCCAAGTCAACATCTCTGAACTTATATATTTAGA 2138  
 Db 1921 GCCTGGGGAATCTCTGACACCCCAAGTCAACATCTCTGAACTTATATATTTAGA 1980  
 Qy 2139 CCATACCAAGGACAGGTACAGGAAATCAATATGATCTCCCTCCCAAAACTTA 2198  
 Db 1981 CCATACCAAGGACAGGTACAGGAAATCAATATGATCTCCCTCCCAAAACTTA 2040  
 Qy 2199 TAAATGCAATTAATGACACAAAGACGCACTTTTGAACAGAGGGGAGAGCTTT 2258  
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 Qy 2259 TTCTGTATATGCTTATATATTAATGCTATAGGCTGTTAAAAAACAAGATTATTTAA 2318  
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 Qy 2319 AATTTAAAGCAAAAAGTCAAAA 2341  
 Db 2161 AATTTAAAGCAAAAAGTCAAAA 2183

RESULT 11  
 US-09-991-073-228  
 ; Sequence 228, Application US/09991073  
 ; Patent No. US20020127576A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Bolstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Baton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerlitsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Kijavlin, Ivar J.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Thomas, Daniel  
 ; APPLICANT: Williams, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: P2730P1C15  
 ; CURRENT APPLICATION NUMBER: US/09/991,073  
 ; CURRENT FILING DATE: 2001-11-14  
 ; PRIOR APPLICATION NUMBER: 60/049787  
 ; PRIOR FILING DATE: 1997-06-16  
 ; PRIOR APPLICATION NUMBER: 60/062250  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/065186  
 ; PRIOR FILING DATE: 1997-11-12  
 ; PRIOR APPLICATION NUMBER: 60/065311  
 ; PRIOR FILING DATE: 1997-11-13  
 ; PRIOR APPLICATION NUMBER: 60/066770  
 ; PRIOR FILING DATE: 1997-11-24  
 ; PRIOR APPLICATION NUMBER: 60/075945  
 ; PRIOR FILING DATE: 1998-02-25

[illegible]



; PRIOR APPLICATION NUMBER: 60/091626  
 ; PRIOR FILING DATE: 1998-07-02  
 ; PRIOR APPLICATION NUMBER: 60/091633  
 ; PRIOR FILING DATE: 1998-07-02  
 ; PRIOR APPLICATION NUMBER: 60/091978  
 ; PRIOR FILING DATE: 1998-07-07  
 ; PRIOR APPLICATION NUMBER: 60/091982  
 ; PRIOR FILING DATE: 1998-07-07  
 ; PRIOR APPLICATION NUMBER: 60/092182  
 ; PRIOR FILING DATE: 1998-07-09

Query Match 92.8%; Score 2171.8; DB 10; Length 2185;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 2176; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 159 GTTCTCTTCCGAGCAAAATCCAGCGATGTGTGAATATGAACTGACCAACATGA 218  
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 Db 1741 CGCAGCGGAGCTGTTGATATATCAGGTGAGCAAGACATCCAGCAACATCCGAG 1800  
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 Db 1801 CAGCAACAGAGCTCCGTCCGCTGTATCAGGTGAAGGGGAGTATGCTGCCAATTC 1860  
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QY 2139 CCCATACCAAGACAGAGTACAGAGAACTCAATATGACTCCCTCCCAAAAACTTA 2198  
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DB 2041 TAAATGCAATGAAATGACACAAAGACAGCACTTTTGTACAGATGGGGAGACTTT 2100  
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DB 2101 TTCTTGATATGCTTATATATTAAGTCTATGGCTGGTTAAAAACATTTATATTA 2160  
QY 2319 AATTTAAAGCAAAAGTCAAAA 2341  
DB 2161 AATTTAAAGCAAAAGTCAAAA 2183

RESULT 12  
US-09-990-442-228  
Sequence 228, Application US/09990442  
Patent No. US20020132252A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Nadel, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C8  
CURRENT APPLICATION NUMBER: US/09/990,442  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607

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PRIOR APPLICATION NUMBER: 60/087609  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087827  
PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
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PRIOR FILING DATE: 1998-06-04  
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APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Matanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C17  
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Query Match 92.8%; Score 2171.8; DB 10; Length 2185;  
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Db AATTTAAGCAAAAAAGTCAAAA 2183

RESULT 14  
US-09-993-604-228  
Sequence 228, Application US/09993604  
Patent No. US20020137075A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
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APPLICANT: Paoni, Nicholas F.  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C25  
CURRENT APPLICATION NUMBER: US/09/993,604  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
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PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
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PRIOR FILING DATE: 1997-11-24  
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PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 92.8%; Score 2171.8; DB 10; Length 2185;  
Best Local Similarity 99.7%; Pred. No. 0;  
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QY 279 TCTACCTGAGGCGGAATGTGATTTCTGTGTGACGACCATGCTGCTCCGCTTCAGCGG 338  
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QY 339 GGGCCCAAGACTGCCCCCTCCGTCTGTGAGTAATCAAGTTGACAGAGGTGTGCA 398  
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QY 399 GCGCCCGGGGCTTCCGAGGTCCCGAGGGTATTCCTTGAACACCCGGTAACCTCAAC 458  
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QY 459 TCATGAGAAACAATCATCAGATGATCCAGGCGGACACCTTCCGACCTCCACACCTG 518  
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RESULT 15  
US-09-990-456-228

Sequence 228, Application US/09990456

Patent No. US20020137890A1

GENERAL INFORMATION:

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C22  
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PRIOR FILING DATE: 1998-07-09

Query Match 92.8%; Score 2171.8; DB 10; Length 2185;  
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QY 219 AGCTCTGTGGCAGTAAGTGTGACACCAACCACTGGAATGCCATCTGCTCCGTTG 278  
DB 61 AGCTCTGTGGCAGTAAGTGTGACACCAACCACTGGAATGCCATCTGCTCCGTTG 120  
QY 279 TCTACTCAGCGCCAGATGTGATCTGTGTGACGACCATGCTGTCCGCTCAGCCG 338  
DB 121 TCTACTCAGCGCCAGATGTGATCTGTGTGACGACCATGCTGTCCGCTCAGCCG 180  
QY 339 GGGCCCAAGACTGCCCTCGCTGCTGTGCACTAACCACTTACGAAAGTGTGTGCA 398  
DB 181 GGGCCCAAGACTGCCCTCGCTGCTGTGCACTAACCACTTACGAAAGTGTGTGCA 240  
QY 399 CGGCGCGGGGCTCTCGAGGTCCCGAGGGTATTCCTGGAACCGGATCACTCAAC 458  
DB 241 CGGCGCGGGGCTCTCGAGGTCCCGAGGGTATTCCTGGAACCGGATCACTCAAC 300  
QY 459 TCATGAGAACACATCATCATGATTCAGGCGGACCACTTCCGCACTCCACCACTG 518

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Qy	579	TGGGCACCTTCAGACCCCTGGAGCTGTTCCGCAACTGGCTGACAGTCACTCCTTAGCGGGG	638
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Qy	639	CCTTGAATACCTGTCGCAAGCTGGCGGGAGCTGTGGCTTCGCAACCCCATCGAAAGCA	698
Db	481	CCTTGAATACCTGTCGCAAGCTGGCGGGAGCTGTGGCTTCGCAACCCCATCGAAAGCA	540
Qy	699	TCCCTCTTTACGCTTCAACCGGGTGCCTCCCTCATGCGCTGGACTTTGGGGAGCTCA	758
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Qy	759	AGAAAGCTGGAGTATATCTCTGAGGGAGCTTTTGAAGGGCTGTTCACCTCAAGTATCTGA	818
Db	601	AGAAAGCTGGAGTATATCTCTGAGGGAGCTTTTGAAGGGCTGTTCACCTCAAGTATCTGA	660
Qy	819	ACTTGGGGCATGTGAACATTTAAAGACATGCCCATCTCACCCCTGGTGGGGGCTGAGG	878
Db	661	ACTTGGGGCATGTGAACATTTAAAGACATGCCCATCTCACCCCTGGTGGGGGCTGAGG	720
Qy	879	AGCTGGAGATGTGAGGGAACCACTTCCCTGAGATCAGGCTCGGCTCTTCANTGGCTGAG	938
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Qy	939	GCTCCCTCCAGAGCTCTGGGTCATGAACTCACAGGTCAAGCTGATTTAGCGGAATGCTT	998
Db	781	GCTCCCTCCAGAGACTCTGGGTCATGAACTCACAGGTCAAGCTGATTTAGCGGAATGCTT	840
Qy	999	TTGACGGGCTGGCTTCACCTGTGGAACTCAACTTGGCCCAATTAACCTCCTCTTTCG	1058
Db	841	TTGACGGGCTGGCTTCACCTGTGGAACTCAACTTGGCCCAATTAACCTCCTCTTTCG	900
Qy	1059	CCCATGACCTTCTTAAACCCCGCTGAGGTACCTGTGTGAGTTGATCATACACCAACCTT	1118
Db	901	CCCATGACCTTCTTAAACCCCGCTGAGGTACCTGTGTGAGTTGATCATACACCAACCTT	960
Qy	1119	GGAACGTGTGATTGACACTTCTGTGTGAGCTAGCCTGTGTGGCTTCGAGAGTATATACCA	1178
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Qy	1299	TCAACATTTCTGAGGGTGGAGTGGCAGAACTTAAGTGTGCGACTTCCCTATGTCTTCG	1358
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Db	1201	TGAAGTGTGTCTGCTCCCATATGGGACAGTGTCTCAGCAGACGCTCCCGCACCAAGAACT	1260
Qy	1419	CTGTCTCTCAAGACGCGCACTTGAACCTTTTCCACAGTGTCTGCTTTCAGACCTGGGGGT	1478
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Qy	1479	ACAACATGATGGGACCAATGTGTGAGGCAACTCCACAGCCTTCGACTTACTCATGTGGA	1538
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[illegible]

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Job time : 773 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 22, 2004, 15:00:44 ; Search time 4855 Seconds  
(without alignments)  
11719.213 Million cell updates/sec

Title: US-09-991-053-9  
Perfect score: 2341  
Sequence: 1 cacttcccccttgcataat.....ttaagacaaagtcacaa 2341

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapect 1.0

Searched: 22781392 seqs, 12152238056 residues  
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
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1: em\_estba:\*  
2: em\_esthum:\*  
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5: em\_estov:\*  
6: em\_estpl:\*  
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9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
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18: em\_gss\_inv:\*  
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20: em\_gss\_vrl:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_man:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	1920.6	82.0	2271	11	BC012209 Mus muscu
2	1259.6	53.8	2833	11	AK046781 Mus muscu
3	712.6	30.4	780	14	CA310827 UI-CF-FNO
4	704.6	30.1	806	9	AV709803 AV709803

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6	628	26.8	1914	11	BC032460 Homo sapi
7	618.6	26.4	11	BC0185392 UI-E-EJ1	
8	604.8	25.8	3494	11	AK032467 Mus muscu
9	603.8	25.8	1845	11	BC053486 Mus muscu
10	603.6	25.8	3097	11	AK034276 Mus muscu
11	603.6	25.7	1133	11	AK048322 Mus muscu
12	600.6	25.7	2873	11	AK032088 Mus muscu
13	570	24.3	883	10	BF165865 Mus muscu
14	565.4	24.2	590	13	BM085165 UI-E-EJ1
15	556.8	23.8	609	13	BQ340625 PMO-NN025
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17	515	22.0	611	13	BE859884 UI-M-AQ1
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19	512.2	21.9	593	14	CA890729 B0161B05-
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21	495.4	21.2	514	13	BQ184873 UI-E-EJ1
22	494.8	21.1	504	13	BQ186663 UI-E-EJ1
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25	476.4	20.4	478	9	AM524479 w126n10.x
26	444.2	19.0	913	13	BM460831 BX460831
27	442.2	18.9	881	12	B1736237 603359928
28	439.4	18.8	447	9	A1435407 tln94b04.x
29	435	18.6	803	12	B1916800 603177924
30	435	18.6	924	13	BX440523 BX440523
31	418	17.9	485	14	CA890728 B0161B05-
32	412.4	17.6	946	12	B1522468 603175417
33	409.4	17.5	487	29	BZ239666 CH230-272
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35	397.6	17.0	424	10	AM954538 EST366608
36	397.6	17.0	710	13	BQ178757 UI-M-EVO-
37	397.4	17.0	793	14	CA315186 UI-M-FWO-
38	395.6	16.9	870	14	CA978880 AGENCOURT
39	393	16.8	509	13	BU789069 1039005.X
40	385.6	16.5	470	12	BM964085 UI-M-EQO-
41	385.4	16.5	926	29	AL219943 Telraodon
42	383.4	16.4	393	3	A1470931 t191c05.x
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45	347.2	14.8	928	10	BG337189 602434283

## ALIGNMENTS

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DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

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BC012209.1 GI:15126555  
HTC.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 2271)  
Strausberg, R.  
Direct Submission  
Submitted (06-NOV-2001) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome  
Sequencing Center  
Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
 Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,  
 Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Munny, D.M.,  
 Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>  
 Series: IRAC Plate: 23 Row: n Column: 10  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: Hexamer frequency ORF  
 analysis, Genomescan gene prediction  
 This clone has the following problem: frame shifted.

## FEATURES

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 /db\_xref="taxon:10090"  
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 arose spontaneously from a senescent normal mammary  
 (clonal) outgrowth infected with the virus MMTV."  
 /clone\_1lb="NCL CGAP\_Lu29"  
 /lab\_host="DH10B"  
 /note="Vector: pCMV-SPORT6"  
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 Matches 2071; Conservative 0; Mismatches 169; Indels 9; Gaps 4;

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 13 CTTCCCACTCTCTCTCAAGTGAAGAGAGCTCTTACCTTAAGCCGGGAG 72  
 154 GGTGCTCTCTCTCTCCGAGCAAAATCCAGCGCATGTGATTAATGAGTCC 213  
 73 GGTGCTCTCTCTCTCCGAGCAAAATCCAGCGCATGTGATTAATGAGTCC 132  
 214 CATGAAGCTCTGTGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 273  
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 274 GTTGTCTAAGTCAAGCGGAGTGTGATTTCTGTGTGCAAGTGTGTGTG 333  
 190 GTGTGTCTAAGTCAAGCGGAGTGTGATTTCTGTGTGCAAGTGTGTGTG 249  
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 250 AGCGGGGCGGAGAGTCTCCCTCCGTCTGTCTGTGAGTGAAGTGAAGT 309  
 394 GTGCAAGCGGCGGAGTCTCTCCGAGTCCGAGGAGTATTCCTTGAACAC 453  
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 430 CTTGAGAGTCTCTGAGTGGGAGAGAACATTCAGAGGCGCAACCTTCCGCA 489  
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 634 CGGCTCTGAGAGTCTCTGAGTGGGAGAGAACATTCAGAGGCGCAACCT 693  
 550 TGGCTCTGAGAGTCTCTGAGTGGGAGAGAACATTCAGAGGCGCAACCT 609

694 AAGATCCCTCTTACGCTTCAACCGGGAGTCCCTCCCTCATGCGCTGAGTGGGGA 753  
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 754 GCTCAAGAGTGAAGTATCTCTGAGGAGCTTTTGAAGGCTGTTCACCTCAAGTA 813  
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Qy      1893 TCACAGCCGCGCGAGCTGTTAGATTAATCCAGGTGAGCGAAGACATCCAGACCAAT 1952
Db      1810 TCACAGCTGCGACGAGCAGTAGAAGTTATCCAGGTGATGAAGACATCCAGACGACAC 1869
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Db      1870 CTGCGAGCAGCAACGACGAGCTCCGTCGGGTGATGAGGTGAGGGGCGAGTGTGTGCCCA 1929
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Db      1990 AAAACAGCCTGGGGAACTCTCTGCAACCCACAGTCAACACTATCTGAACTTATATA 2049
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Qy      2193 AACTTAATAANTGATGAATGAATGACACAAAGACAGAACTTTGTACAGAGTGGGAGA 2252
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Db      2225 TATTAAATTTAAAGACAAAGTCAAAA 2253

RESULT 2
AK046781
LOCUS
DEFINITION
AK046781 2833 bp mRNA linear HTC 05-DEC-2002
Mus musculus 10 days neonate medulla oblongata cDNA, RIKEN
full-length enriched library, clone: B83005D03 product: LIBC-LIKE
PROTEIN (FRAGMENT) homolog [Mus musculus], full insert sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
Carninci, P. and Hayashizaki, Y.
TITLE
High-efficiency full-length cDNA cloning
JOURNAL
MEDLINE
99279253
PUBMED
10349636

REFERENCE
AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL
MEDLINE
20499374
PUBMED
11042159

REFERENCE
AUTHORS
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, U., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M.,
Sun, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kaishogi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsuhi, M.,

```

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TITLE
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
JOURNAL
MEDLINE
20530913
PUBMED
11076861

REFERENCE
AUTHORS
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S.,
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamataka, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadoya, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Fleischmann, M., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G.,
Quackenbush, J., Schriml, L.M., Staudt, F., Suzuki, R., Tomita, M.,
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Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Guernicich, S., Hill, D.,
Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P.,
Marchionni, L., Mashima, J., Mazzarelli, J., Mombaearte, P., Nordone, P.,
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schombach, C., Seta, T., Shibata, Y., Storch, K.F., Suzuki, H.,
Toyo-oka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L.,
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohetsuki, S.
and Hayashizaki, Y.

TITLE
Functional annotation of a full-length mouse cDNA collection
JOURNAL
MEDLINE
21085660
PUBMED
11217851

REFERENCE
AUTHORS
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL
MEDLINE
Nature 420, 563-573 (2002)
AUTHORS
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
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Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shitaki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.

TITLE
Direct Submission
JOURNAL
MEDLINE
Submitted (16-UTL-2001) Yoshinide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration and Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
Location/Qualifiers
1. 2833
/organism="Mus musculus"
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BASE COUNT 791 a 649 c 685 g 708 t

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 61 AGCTCCCTCAAGAACTCTGGGTGATGAACTCAAGAGTCAAGCTGATGAGGGAATGCT 120  
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 1118 TGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1177  
 241 TGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
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 301 AATTCACCTGCTGTGCGCTGTGATGCTCCCATGACATGACGAGGCGCTACCTGCTG 360  
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 1358 GTGAAGTGTGCTGCGCCATGAGGACAGTGTCTACGCCAGCTCCCGGCATCCCGGATC 1417  
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 1418 TCTGTCTCAACAGAGGACCTTGAACCTTTCCACGCTGCTTTCAGACATGAGGCTG 1477  
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 1478 TACACATGATGAGGACCAATGTTGACAGAACTCAAGGCTGGCTTACCTCAATGGG 1537  
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661 AGCTGGCCGAGCTCAACACCCCCCACTTCTTTCACACATGATGAGGAAACC 720  
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 781 GGTTCACAGCCGAGATATACACCTCTTACACAGGCTGTCTTACAGCTCCACT 840  
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 841 AAGAGGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
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 1436 AATTTTAAAGCAAAAAGTCAAAA 1459

RESULT 3  
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 DEFINITION  
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 CA310827  
 ACCESSION  
 VERSION  
 CA310827.1 GI:24528925  
 KEYWORDS  
 EST.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS  
 Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL  
 Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE  
 97044477



PUBMED  
COMMENT

8889548  
Contact: McCray, PB  
McCray Lab  
University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171  
Email: paul-mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).  
The following repetitive elements were found in this cDNA sequence: 1-58, >POLY\_A#simple\_repeat (matched compliment) 386-416, >(CAG)n#simple\_repeat (matched compliment)  
Seq primer: M13 FORWARD  
POLYA=yes.

FEATURES  
source

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/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; UI-CF-FNO is a subtracted cDNA library derived from two normalized Human lung epithelial cell libraries (EN1 and DU1) The library was subtracted according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact: bento-soares@uiowa.edu  
TAG LIB=UI-CF-FNO  
TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS 6hr to LPS 24h  
TAG\_SEQ=CTGCTCAGCT"  
BASE COUNT 154 a 161 c 207 g 257 t 1 others  
ORIGIN

Query Match 30.4%; Score 712.6; DB 14; Length 780;  
Best Local Similarity 98.8%; Pred. No. 5.3e-138;  
Matches 759; Conservative 0; Mismatches 5; Indels 4; Gaps 4;

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DB 422 ACATCCAGCAGCAACATCCGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 363  
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DEFINITION AV709803 ADC Homo sapiens cDNA clone ADCAPC04 5', mRNA sequence.  
ACCESSION AV709803  
VERSION AV709803.1 GI:10727827  
KEYWORDS EST.  
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ORGANISM Homo sapiens (human)  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 806)  
Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Jia, J., Ren, S., Zhong, M., Lu, G., Hu, R., Chen, J., Chen, Z., and Han, Z.  
Homo sapiens cDNA ADC clones  
Unpublished  
Contact: Zeguang Han  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China  
Tel: 86-21-50801919 (ex.45)  
Fax: 86-21-50801922  
Email: hanzg@chgc.sh.cn  
This clone is available at CHGC in Shanghai.  
Location/Qualifiers  
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FEATURES  
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ORIGIN

Query Match 30.1%; Score 704.6; DB 9; Length 806;  
Best Local Similarity 95.3%; Pred. No. 2.5e-136;  
Matches 759; Conservative 0; Mismatches 34; Indels 3; Gaps 3;

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RESULT 5
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LOCUS UI-CF-EN1-acv-a-12-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
DEFINITION UI-CF-EN1-acv-a-12-0-UI 3', mRNA sequence.
ACCESSION BM975435
VERSION BM975435.1 GI:19593026
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 711)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery.

```

## JOURNAL

Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 PUBMED 8889548  
 COMMENT Contact: McCray, PB  
 McCray Lab  
 University of Iowa  
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
 Tel: 319 356 4866  
 Fax: 319 356 7171  
 Email: paul-mccray@uiowa.edu  
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com) or from Open Biosystems  
 (www.openbiosystems.com).  
 The following repetitive elements were found in this cDNA  
 sequence: 1-58, >POLY A#simple repeat (matched complement) 386-416,  
 >(CAG)n#simple repeat (matched complement)  
 Seq primer: M13 FORWARD  
 POLYA=yes.

## FEATURES

## SOURCE

Location/Qualifiers  
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 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_lib="UI-CF-EN1"  
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I; UI-CF-EN1 is a normalized cDNA library containing the following tissue(s): Primary Lung Cystic Fibrosis Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CTGCTCAGGT.  
 TAG LIB=UI-CF-EN1  
 TAG TISSUE=Human Lung Epithelial Cell lines untreated LPS 6hr to LPS 24h  
 TAG SEQ=CTGCTCAGGT"

## BASE COUNT

145 a 188 g 234 t

## ORIGIN

Query Match 28.7%; Score 672.4; DB 12; Length 711;  
 Best Local Similarity 99.6%; Pred. No. 1.3e-129;  
 Matches 695; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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Qy 1645 TACCAGTCACTGCTTACCAAGCGGATATACCACTTACCAAGCTGCTCATTCAGAC 1704
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Qy 1765 CAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1824
Db 592 CAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 533
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[illegible]

QY 1039 CAATTAACCTCTCTTTTGGCCCATGACCTCTTTACCCCGGTGAGGATCCTGTGGAGTT 1098  
 DB 870 CAACAACCTGATGTCGTGCCCCCAAGACCTCTTCAACGCCCTTGACCGCTCGAGCGGT 929  
 QY 1099 GCATCTACACCAACCTTGGAACTGATGATGACATTTCTGTGGCTAGCTGTGGCT 1158  
 DB 930 GCACCTCAACCAACACCTTGGCAATGCACTGGCACTGTCTGTGGCTAGCTGTGGCT 989  
 QY 1159 TCGAGATATATACCAACCAATTCACCTGTGTGGCCGCTGTATGCTCATGACAT 1218  
 DB 990 CAAGAGACGGTGGCCAGCAACGACCTGCTGCGCCGCTGTATGCGCCCGCGCT 1049  
 QY 1219 GCGAGCGCTACCTCTGTGAGGTGAGACGAGCCCTCTTCAAGTCTGTGCTTCTAT 1278  
 DB 1050 CAAGGGGGCTACATTTGGGAGCTGAGACAGTCCGATTTCACTGTCTATGCGCCGTCAT 1109  
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 QY 1456 GCTGCTTCAACACATGAGGTGTATCATGATGAGGACCAATGTGAGGCACTTCA 1515  
 DB 1290 CACCGTGAGACACGCGGCAAGTACAGTGATGTCGAACTCAACGCGCAACACAC 1349  
 QY 1516 CGCCTCGGCTACCTCAATG 1535  
 DB 1350 CGCCTCGGCTACCTCAACG 1369

RESULT 7  
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 LOCUS B0185392  
 DEFINITION UI-E-E11-aj-u-f-24-0-UI-81 UI-E-E11 Homo sapiens cDNA clone  
 ACCESSION B0185392  
 VERSION B0185392.1 GI:20360943  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 664)  
 Reference: Ronaldo, M.F., Lennon, G. and Soares, M.B.  
 Title: Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 Journal Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 PUBMED 8889548  
 COMMENT Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@uiowa.edu  
 Tissue Procurement: Dr. Gregg Hageman  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com).  
 The following repetitive elements were found in this cDNA  
 sequence: 1-72, >POLY\_A#Simple\_repeat (matched complement) 399-429,  
 >(CAG)n#Simple\_repeat (matched complement)  
 Seq primer: M13 FORWARD

FEATURES  
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 location/Qualifiers  
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 optic nerve, retina, Retina Foveal and Macular, RPE and  
 Choroid"  
 /dev\_stage="fetal and adult"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_lib="UI-E-E11"  
 /note="Organ: eye; Vector: pRTT3-Pac (Pharmacia) with a  
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 UI-E-E11 is a subcloned cDNA library constructed  
 according to Ronaldo, Lennon and Soares, Genome Research,  
 6:791-806, 1996. First strand cDNA synthesis was primed  
 with an oligo-dT primer containing a Not I site. Double  
 stranded cDNA was ligated to an EcoR I adaptor, digested  
 with Not I, and cloned directionally into pRTT3-Pac  
 vector. The oligonucleotide used to prime the synthesis of  
 first-strand cDNA contains a library tag sequence that is  
 located between the Not I site and the (dT)18 tail. The  
 sequence tags for this library are: fetal eyes, AGAATCAAGA  
 ; lens, CGATTAGCGA; eye anterior segment, AATGCCGAT;  
 optic nerve, CCATTAGTGT; retina, CCGCG; Retina Foveal and  
 Macular, GTCC; RPE and Choroid, CCGTA. This library was  
 created for the program, Gene Discovery in the Visual  
 System, supported by National Eye Institute (NEI).  
 TAG\_LIB=UI-E-E11  
 TAG\_TISSUE=Foveal and Macular Retina  
 TAG\_SEQ=GTCC"

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 Matches 621; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
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 DB 653 CACAGGGGTGGCACTACCCGCGACAGACACCACTGACAAAGTGCAGCCGCTGATGA 594  
 QY 1777 AGTCATGAAGCCACCAAGATTCATTTGCTGCTGTGGAGTACCTGTAGCTGC 1836  
 DB 593 AGTCATGAAGCCACCAAGATTCATTTGCTGCTGTGGAGTACCTGTAGCTGC 534  
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 DB 533 CGCCATGTTATGTTCTTATTAATCTTGAAGCGGCACAGAGCGGAGTACAGTCA 474  
 QY 1897 AGCCGCGCGACCTGTAGTATATCCAGGTGACGAAGACATCCAGCAGCAATCCG 1956  
 DB 473 AGCCGCGCGACCTGTAGTATATCCAGGTGACGAAGACATCCAGCAGCAATCCG 414  
 QY 1957 AGCAGCAACGACGCTCGTCCGCTGATCAGGTGAAGGGGAGTAGTGTGCCCAAT 2016  
 DB 413 AGCAGCAACGACGCTCGTCCGCTGATCAGGTGAAGGGGAGTAGTGTGCCCAAT 354  
 QY 2017 TCATGACCATATTAATCAACAACCTTCAACAACGACGACATGGGGCCACTGACAGAAA 2076  
 DB 353 TCATGACCATATTAATCAACAACCTTCAACAACGACGACATGGGGCCACTGACAGAAA 294  
 QY 2077 CAGCTGGGGAATCTCTGCAACCCCAAGTCACCATATCTTGAACCTTATATATCA 2136  
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Oy	2257	TTTTCTGTATATGCTTATATATTTATTTAGTCTATGCGCTGGTTAAAAAACAAGATTATTT	2316
Db	113	TTTTCTGTATATGCTTATATATTTATTTAGTCTATGCGCTGGTTAAAAAACAAGATTATTT	54
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Db	53	AAAATTTTAAACAAAAAGTCNAAA	29
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DEFINITION	Mus musculus adult male olfactory brain cDNA, RIKEN full-length		linear
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	TUMOR ASSOCIATED PROTEIN NAG14 [Homo sapiens], full insert		
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ACCESSION	AKO32467		
VERSION	AKO32467.1	GI:26328286	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
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	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE			
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
PUBMED	99279253		
REFERENCE	10349636		
AUTHORS			
TITLE			
JOURNAL	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,		
PUBMED	Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
REFERENCE	Normalization and subtraction of cap-trapper-selected cDNAs to		
	prepare full-length cDNA libraries for rapid discovery of new genes		
	Genome Res. 10 (10), 1617-1630 (2000)		
JOURNAL	2049374		
PUBMED	11042159		
REFERENCE			
AUTHORS			
TITLE			
JOURNAL	Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,		
PUBMED	Kono, H., Akiyama, Y., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,		
REFERENCE	Sun, N., Ishii, Y., Nakamura, S., Hazama, M., Nishim, T., Harada, A.,		
	Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaishigaki, K.,		
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	Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
	RIKEN Integrated Sequence Analysis (RISA) system-384-format		
	sequencing pipeline with 384 multiplexed sequencer		
	Genome Res. 10 (11), 1757-1771 (2000)		
JOURNAL	20530913		
PUBMED	11076861		
REFERENCE			
AUTHORS			
TITLE			
JOURNAL	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,		
PUBMED	Aikawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S.,		
REFERENCE	Aikawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamataka, I.,		
	Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kaenkawa, T., Saito, R.,		
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	Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,		
	Plancher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,		
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	and Hayashizaki, Y.		

TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409 (6821), 685-690 (2001)  
MEDLINE 21085660  
PUBMED 11217851  
REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)  
(bases 1 to 34,94)

REFERENCE 6

AUTHORS Aochi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carrinci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hayamto, K., Hiraoka, T., Hiroane, T., Hori, F., Imclan, K., Ishii, Y., Itoh, M., Kigawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohnato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Saeki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshinobu Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-1-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genomics-res@gsc.riken.go.jp).  
URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: <http://genome.gsc.riken.go.jp/>.  
URL: <http://fantom.gsc.riken.go.jp/>.  
location/Qualifiers

SOURCE 1. 3494

FEATURES

source

organism="Mus musculus"  
mol\_type="mRNA"  
strain="C57BL/6J"  
db\_xref="FANTOM\_DB:6430556C10"  
db\_xref="taxon:10090"  
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3470..3475  
/note="putative"







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RESULT 10  
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 LOCUS  
 DEFINITION Mus musculus adult male diencephalon cDNA, RIKEN full-length  
 enriched library, clone:9330171H21 product:weakly similar to BRAIN  
 TUMOR ASSOCIATED PROTEIN NAG14 [Homo sapiens], full insert  
 sequence.  
 ACCESSION AK034276  
 VERSION AK034276.1 GI:26329834  
 KEYWORDS HTC; CAP trapper.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 1 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning  
 Meth. Enzymol. 303, 19-44 (1999)  
 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL MEDLINE 20499374  
 PUBMED 11042159  
 REFERENCE  
 3  
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
 Konno, H., Akiyama, Y., Nishi, K., Kitasuna, T., Tashiro, H., Itoh, M.,  
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,  
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 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Onara, E., Watanabe, M.,  
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multiplexed sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL MEDLINE 20530913  
 PUBMED 11076861  
 REFERENCE  
 4  
 AUTHORS Kawai, J., Shingawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,

Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,  
 Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamataka, I.,  
 Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,  
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 Toyooka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L.,  
 Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Konturki, S.,  
 and Hayashizaki, Y.  
 Functional annotation of a full-length mouse cDNA collection  
 Nature 409 (6821), 685-690 (2001)

TITLE  
 JOURNAL MEDLINE 21085660  
 PUBMED 11217851  
 REFERENCE  
 5  
 AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 6 (bases 1 to 3097)  
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,  
 Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kaga, I., Kasukawa, T.,  
 Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
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 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
 Muramatsu, M., and Hayashizaki, Y.  
 Direct SubMISSION  
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,  
 URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,  
 Fax: 81-45-503-9216)  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.go.jp/  
 URL: http://fantom.gsc.riken.go.jp/  
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 ACCESSION  
 AK048322  
 VERSION  
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 HTC; CAP trapper.  
 SOURCE  
 Mus musculus (house mouse)

ORGANISM	Mus musculus
REFERENCE	Mammalia; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteleostomi; Rodentia; Scuriongnathi; Muridae; Murinae; Mus.
REFERENCE	1 Carninci, P. and Hayashizaki, Y.
JOURNAL	High-efficiency full-length cDNA cloning
MEDLINE	Meth. Enzymol. 303, 19-44 (1999)
PUBMED	99279253
PUBMED	10349636
REFERENCE	2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE	3
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, N., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Obara, E., Matsumi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	4
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., Aizawa, K., Iizawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamataka, I., Saito, T., Okazaki, Y., Gojohori, T., Bono, H., Kasukawa, T., Saito, R., Kado, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochava, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L. M., Stanbly, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Kono, H., Bardelli, R., Barin, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombert, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyokawa, K., Wang, K. H., Weltz, C., Whitaker, C., Wilming, L., Wyshaw-Borja, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S., and Hayashizaki, Y.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409 (6821), 685-690 (2001)
MEDLINE	21085660
PUBMED	11217851
REFERENCE	5
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
MEDLINE	6 (bases 1 to 3133)
PUBMED	12108560
REFERENCE	6
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagata, T., Hara, A., Hashimoto, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Koyu, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, K., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sato, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaki-Akai, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

TITLE	Direct Submission
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suenho-cho, Tsukuba, Ibaraki, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/ Location/Qualifiers
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 DB 2805 TGATGCTGTGATTTCTTACAGATGAGGAACAGCACTCGGCAAAACCACTATGCTC 2864  
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 DB 2865 CAACAAGACTTGTGAATCATTAAGTGTATGATGATGATGATGATGATGATGATGATGAT 2920

RESULT 12  
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 TUMOR ASSOCIATED PROTEIN MAG14 (Homo sapiens), full insert  
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 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
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 AK032088.1 GI:26082676  
 HTC; CAP trapper.  
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 1 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning  
 Meth. Enzymol. 303, 19-44 (1999)  
 99279253  
 10349636

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 Genome Res. 10 (10), 1617-1630 (2000)  
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REFERENCE  
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 TITLE  
 JOURNAL  
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 3 Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,  
 Komno, H., Akiyama, J., Nishi, K., Katsunari, T., Tashiro, H., Itoh, M.,  
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 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, D.,  
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format  
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 Genome Res. 10 (11), 1757-1771 (2000)  
 20530913  
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REFERENCE  
 AUTHORS  
 4  
 Kawai, J., Shingawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,  
 Arakawa, T., Hara, A., Fukunishi, Y., Komno, H., Adachi, J., Fukuda, S.,  
 Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I.,  
 Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,  
 Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,  
 Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,  
 Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G.,  
 Quackenbush, J., Schiraldi, L. M., Staudt, F., Suzuki, R., Tomita, M.,  
 Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,  
 Baldarelli, R., Barsch, G., Blake, J., Boffelli, D., Bojunga, A.,  
 Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bull, C.,  
 Fletcher, C., Fujita, M., Gariboldi, M., Guestinich, S., Hill, D.,  
 Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,  
 Marchionni, L., Mashima, J., Mazarrelli, J., Mombarts, P., Nordone, P.,

Ring, B., Schinwald, M., Rodriguez, I., Sakamoto, N., Saeki, H., Sato, K., Srinobashi, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyochika, K., Wang, K. H., Weitz, C., Wiltbrecht, C., Wilmink, L., Wydenha-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohzuki, S. and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection  
Nature 409 (6821), 685-690 (2001)

Db	2112	ACACGTGATGAGTGAATTCCTGTGGCAACACCACTGTTCTGCGACCTGGAATGTTA	2171
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ACCESSION	BF165865
VERSION	GI:11046217
KEYWORDS	BF165865.1
SOURCE	EST.
ORGANISM	Mus musculus (house mouse)
	Mus musculus

REFERENCE  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

**AUTHORS** NIH-MGC <http://mgc.nci.nih.gov/>.  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished  
**COMMENT** Contact: Robert Strausberg, Ph.D.

Email: [CGAPDS-i@omail.nih.gov](mailto:CGAPDS-i@omail.nih.gov)  
Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LIML at:  
<http://image.llnl.gov>  
Plate: LIM9215 row: 0 column: 23  
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Stem cell origin."
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VERSION	BQ185165.1 GI:20360716
KEYWORDS	EST.
SOURCE	Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 590)  
 AUTHORS Ronaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 PUBMED 8889548  
 COMMENT Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: Bento-soares@uiowa.edu  
 Tissue Procurement: Dr. Gregg Hageman  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com).  
 The following repetitive elements were found in this cDNA  
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FEATURES  
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 according to Ronaldo, Lennon and Soares, Genome Research,  
 6:791-806, 1996. First strand cDNA synthesis was primed  
 with an oligo-dT primer containing a Not I site. Double  
 stranded cDNA was ligated to an EcoR I adaptor, digested  
 with Not I, and cloned directionally into pT73-Pac  
 vector. The oligonucleotide used to prime the synthesis of  
 first-strand cDNA contains a library tag sequence that is  
 located between the Not I site and the (dT)18 tail. The  
 sequence tags for this library are: fetal eyes, AGAATCAAGA  
 ; lens, CCAATGACCA; eye anterior segment, AATGCCGAT;  
 optic nerve, CCAATGATG; retina, CCGCG; Retina foveal and  
 Macular, GTCC; RPE and Choroid, ACCCTA. This library was  
 created for the program, Gene Discovery in the Visual  
 System, supported by National Eye Institute (NEI).  
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 TAG\_TISSUE=human retina  
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 DB 401 GCAGCAGCAACAGAGCTCCGTCGGTGATCATAGTGAAGGGCAGTAGTCTGCCACA 342  
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 REFERENCE 1 (bases 1 to 609)  
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.U.  
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 MEDLINE 20202663  
 PUBMED 10737800  
 COMMENT Contact: Simpson A.U.J.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM0&cl=PM0-NN0258-  
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 Location/Qualifiers

FEATURES

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No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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Matches 582; Conservative 0; Mismatches 22; Indels 2; Gaps 1;

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